

FIGURE 1

CGGACGCGTGGGTGCGAGGCCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA
CCTGGTGCACCACCACC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
GTTTTCCACCAGCTTTTACCAAGGCCTCCCCTGTTGTGAAGAATTCCATCACGAAGAATCA
ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA
GAACTGGCCAAGAAGCTCAAAGAGGCAGCATTGGAACCATCGATGGAAAAAATATTTAAATTT
GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
ATGTCAAGGATAGAATTCATTCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACTTCATGATGAGAGGCTCTTG
GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT
GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC
AGCTGGCATTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCCAAGTAAAAAGTTTCTGA
ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCCTCATTGGGATCTATG
TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT
AGTTCCTTTTTCAGCATGTTCCCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
ACATTAAATATATTTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAA**ATG**
AAGTGAICTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTTAAATGGGGCAGATATGC
ATTAAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA
TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGT
AATCCTCTCCCAAATAAGCACACACATTTTCAATTCTCATGTTTGAGTGATTTTAAATGTT
TTGGTGAATGTGAAAACATAAGTTTGTGTCATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
TTTAGTAGGTTCACTGAGTAACATAAATTTAGCAAACCTGTGTTTGCATATTTTTTTGGAGT
GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAGAGAGAAG
GAGTCACCTGCAGTCTTTTGTTTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA
GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAAACAAGTGGTCATTGTTACATTCATTT
GCTGAACTTAACAAAACGTTCATCCTGAAACAGGCACAGGTGATGCATTCTCCTGCTGTTG
CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCATGTTTGAAGTTGTACAGAATGTTAATC
ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTTACTTTTGAATGTTACAAAAGGAA
ATAACTTTAAACATATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAG
AATACAAACAGTATACTCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWVAVAGGAAGVGLGALCYGGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSIAIAISRTPVLMNFMMRGWSVTIGVTFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCCGCCCGTCTCCGCCTTCTGCA
CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCCGGCCGCTCGTGAGGG
GGTCGGCACGGGGAGTCGGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTCTGAAG**ATG**TCGG
ACATCGGAGACTGGTTCAGGAGCATCCCGGCGATCACGCGCTATTGGTTCGCCGCCACCGTC
GCCGTGCCCTTGGTCGGCAAACCTCGGCCTCATCAGCCCGGCCTACCTCTTCCTCTGGCCCGA
AGCCTTCCTTTATCGCTTTTCAATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG
GTCCAGGAACCTGGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTCTACGCGA
CTTGAAACAGGAGCTTTTGTGAGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTAACTG
GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCTCTGATCA
TGTCAGTACTTTATGTCTGGGCCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGA
ACACGATTTAAGGCCTGCTATTTACCTGGGTATCCTTGGATTCAACTATATCATCGGAGG
CTCGGTAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTTCTTAATGTTCA
GATACCCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG
CTGCCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGC
TGCTGATCAGAATGGCGGAGGCGGGAGACACAACCTGGGGCCAGGGCTTTCGACTTGGAGACC
AGTGAAGGGGCGGCCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCTCTCCAGTGCTGGGTG
CACTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTT
AGTACGAGACAAAGTTTTCTTAAATCCCGAAGAAATATAAGTGTTCACAAAGTTTCAGAT
TCTCATTTCAAGTCCTTACTGCTGTGAAGAACAATAACCAACTGTGCAAAATGCAAACTGAC
TACATTTTTTGGTGTCTTCTCTTCTCCCCTTTCCGTCTGAATAATGGGTTTTAGCGGGTCCCT
AATCTGCTGGCATTGAGCTGGGGCTGGGTACCAAAACCCTTCCCAAAGGACCTTATCTCTT
TCTTGACACATGCCTCTCTCCCACTTTTCCCAACCCCACTTTGCAACTAGAAAAAGTTG
CCCAAAAATTGCTCTGCCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGT
ACAACAATCATATTCACGTTATTTTCCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAG
AAGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATTGCTTCGACTGACATCCGTTGTT
AACCCTTTGCCACTCTTCAGATATTTTTTATAAAAAAGTACCCTGAGTTTATGAGGGCCA
CAGATTGGTTATTAATGAGATACGAGGGTTGGTGTCTGGGTGTTTGTTCCTGAGCTAAGTGA
TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCC
TTTGCGTTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGT
TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG
ATTCCCATTTCATCTCATTCTGGATATGTGTTTATTGAGTAAAGGAGGAGAGACCCTCATA
CGCTATTTAAATGTCACTTTTTTGCCTATCCCCCGTTTTTTGGTTCATGTTTCAATTAATTGT
GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA
AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGGGGTGTGTTA
TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTT
TCGTAGGTGGGCTTTTTCTATCAGAGCTTGGCTCATAACCAAATAAAGTTTTTTGAAGGCCA
TGGCTTTTACACAGTTATTTTATTTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
ATTGAGTGGCTGTCACACTTTGAGGCAACTAAAAAGGCTTCAAACGTTTTGATCAGTTTCTT
TTCAGGAAACATTTGTGCTCTAACAGTATGACTATTCTTTCCCCCACTCTTAAACAGTGTGAT
GTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTTCTCATTTTGAATAGAGTTTGTGTG
TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACTGTCA
TGTTTTGTTGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAATAATTTAGAGGCCATTACT
CCAATTATGTTGCACGTACACTCATTGTACAGGCGTGGAGACTCATTGTATGTATAAGAATA
TTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTACCCTCTTACCAGTCAGCTGCCTGCGAG
CAGTCATTTTTTCTTAAAGGTTTACAAGTATTTAGAACTTTTCAGTTTCAGGGCAAAATGTTT
ATGAAGTTATTCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTTGTCTGGATT
ATGTTTCTGGAATAATTTTACCAAACAAGCTATTTGAGTTTTGACTTGACAAGGCAAAACA
TGACAGTGGATTCTCTTTACAAATGGAAAAAATAATCCTTATTTTGTATAAAGGACTTCCC
TTTTTGTAACATAATCCTTTTTTATTGGTAAAAATTGTAAATTAAATGTGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGLISPAYLFLWPEAFLYRFQIWRPITATFYF
 PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
 LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
 MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRLL
 GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

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FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
CCTTGTGGCCCAAAGGCCTAACCGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTTGCC
CCTTTGGGGCGGG**ATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
CGGGGTTCCCTGCGAGGCCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
GGCCTGTGTTCCCCTTGTTTTTGGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAGGC
CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
AAACATTGAAATGCAGCTGCAAGCCATTCGAATAATTCAAGAGAGAAATGGTGTATTACCT
GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
GAGGGAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
AATAATTCCTCAAGGGGATGGTGAACATTTTGCACACCCACCTCAGAAGTTAAAATGCATTT
TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGTCTGAAACTTCCTCCCTCC
CACAAAAGGCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
CTTACACTG

FIGURE 6

MAAEEDEVEWVVESIAGFLRGPDSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTIONPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMLQAIIRIIQERNGLVPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAAEKQTLLKRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

GGGCACAGCACATGTGAAGTTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAAGTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTTCGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAAAGAGGAATATGACCAGGAA

The diagram illustrates the experimental setup for measuring the time delay of a quantum state. A laser beam enters from the left, passes through a lens, and is focused onto a sample. The sample is mounted on a stage that can move vertically. A detector is positioned to the right of the sample, and a lens is used to focus the light from the sample onto the detector. The diagram is labeled with various components and their positions.

CGCTGGTTTTTTGTCTCTGCAATATAGGCGGCTTAGAGGGAGGGGCTTTTTTCGCCTATACCTACTG
TAGCTTCTCCACGTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAATAAAC
AGTGGAAATGGAATAACAGTGTCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATAC
ATTCTTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
CTGCCAATGAAGAAAACAAGTATGATTATCTTCCACTACTGTGAATGTGTGCTCAGAACTG
GTGAAGCTAGTTTTCTGTGTGCTTGTGTCAATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
AAATTTGAAATATGCTTCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCCTGCC
TTCTTTATTTCTGATAACTTGATTGTCTTCTATGTCCTGTCCTATCTTCAACCAGCCATC
GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAAGGATAGTGTGAA
GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCT
TGACTGCCGGGACTAAACTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCC
TTTTTCAGCCCTTCCAATTCTGCTTCTTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG
TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTC
ACATCCGCTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTTCTTCAATGGCT
AATATCTATAATGAAAAGATACTGAAGGAGGGGAACCAGCTCACTGAAAGCATCTTCATACA
GAACAGCAAACCTCTATTTCTTTGGCATTCTGTTAATGGGCTGACTCTGGGCCTTCAGAGGA
GTAACCGTGATCAGATTAAGAAGTGTGGATTTTTTTTATGGCCACAGTGCATTTTCAGTAGCC
CTTATTTTTGTAACTGCATTCAGGGCCTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
CATGTTCCATGTCTTGATGGCCAGGTTACCACTGTCAATTATCACAACAGTGTCTGTCTCTGG
TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGGAAGCCCCATCAGTCCTTCTCTCTATA
TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGAATACGCACCTAGGCAAGAAAGGATCCG
AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCA
GCTCTCTTGAACCTTATTTTCACATTTTCAGTGTGTGTAATATTTATCTTTTCACTTTGATA
AACCAGAAATGTTTCTAAATCCTAATATTTCTTTGCATATATCTAGCTACTCCCTAAATGGTT
CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTCTAAAGAACTGATACAGGAGTAACA
ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
TTTCCCTTGGCCTTCAAGCTTCCAAAAAACTTGTAATAATCATGTTAGCTATAGCTTGTATAT
ACACATAGAGATCAATTTGCCAAATATTCACAAATCATGTAGTTCTAGTTTACATGCCAAAGT
CTTCCCTTTTTTAACATTATAAAAGCTAGGTTGTCTCTTGAATTTTGAGGGCCCTAGAGATAGT
CATTTTGCAAGTAAAGAGCAACGGGACCCTTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
CTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAAATATTTTGCTGAAGAAGCAGT
TTCTCAGACACAACATCTCAGAATTTTAATTTTTAGAAATTCATGGGAAATTGGATTTTTGT
AATAATCTTTTGATGTTTTAAACATTGGTTCCCTAGTCACCATAGTTACCACTTGTATTTTA
AGTCATTTAAACAAGCCACGGTGGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT
GTCATTACTCCTGAATTATTACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACT
AATTCAAGCTGTGACTATTGTATATCTTCCAAGAGTTGAAATGCTGGCTTCAGAATCATAC
CAGATTGTCAGTGAAGCTGATGCCTAGGAACCTTTTAAAGGGATCCTTTCAAAGGATCACTT
AGCAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAAAGACC
AGTAATATATAAGTCACTTTACAGTGCTACTTCACACTTAAAGTGCATGGTATTTTTCATG
GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAAGGTGATAGATGATATTAA
AAATTAGCAAAACAAAGTGACTTTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAAGTGGG
CTTTAACTGGCAGGCCTGTATGTTTACAGACTACCATACTGTAAATATGAGCTTTATGGTGT
CATTTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
AGGTAATATACTATTATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAATTG
GTGGAAATTTGTAATTAATAAATTATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI
YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESDDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAACAGTGGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGCTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACCTTA

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FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGCGGCC
GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCTGCGGGGCGAGAGGAGCAT
CCCGTCTACCAGGTCCCAAGCGGCGTGGCCCCGCGGGTTCATGGCCAAAGGAGAAGGCGCCGAG
AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCCCCGGCCCA
GGTGAAGAAAGAACCAGAAAAAGAAACAACAGTTGTCTGTTTGCAACAAGCTTTGCTATG
CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC
CTATTGGATGTTGGCTCAGGTGGGCCCTTTCTCTGCCTCCATCATCCTGTTTGTGGGCCGAGC
CTGGGATGCCATCACAGACCCCTGGTGGGCCTCTGCATCAGCAAATCCCCCTGGACCTGCC
TGGGTCGCCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCCGTCATTGCCTACTTCCTC
ATCTGGTTTCGTGCCCGACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
CTTTGAAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
AGTGCTGGGACGCGGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCCTTGTTTCCAGG
ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATAACATGGCACCACCTTCACAC
AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTTCATTGTCTGTATCTATATAATCTG
TGCTGTTCATCCTGATCCTGGGCGTGGCGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTG
AGCCAATCGCCTACTTCCGGGGCCTACGGCTGGTTCATGAGCCACGGCCCATAACAACTT
ATTACTGGCTTCCTCTTCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAAGTTTGTCTTGTT
TTGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCT
CGGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT
GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
TACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
GGAACCGAGCCCATCTTCTTCTCCTTCTATGTCTTCTTACCAAGTTTGCCTCTGGAGTGTC
ACTGGGCATTTCTACCCTCAGTCTGGACTTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC
CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG
CTGGGCCTGCTGCTCTTCAAAATGTACCCCATTTGATGAGGAGAGGCGGCGGCAGAATAAGAA
GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
AGCTGGCTAGCATCCTCTAGGGCCCCGCCACGTTGCCCCAAGCCACCATGCAGAAGGCCACAG
AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
CTGAAGACTCAAGGAGGTGGCCCAGGACACTTGCTGTGCTCACTGTGGGGCCGGCTGCTCTG
TGGCCTCCTGCCTCCCCTCTGCCTGCCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGAATA
TGCCAAGGACTGATCGGGCCTAGCCCAGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC
TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTGTATGTATATGTCTGTGAGCTA
TTAATGTTATTAATTTTCATAAAAGCTGGAAAGC

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FIGURE 12

MWLRWALS LPPSSCLWAE PGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHTARPIGT CFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQQQIVGQADTPCFQDFNSSTVASQSANHHTGTTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAAQQSEPIAYFRGLRLVM SHGPYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNL LLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLG LLLFKMYPIDEERRRQNK KAL
QALRDEASSSGCSETDSTELASIL

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FIGURE 13

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATAACATCAAACCTTA
TACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
ATGAGCAGGTCTGAAGACTAACATTTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGT
GGTGGTTTTAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
CAGTTTTATGCATTGCTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTACTGAGTTGTTTAGG
ACTTTCCTATTGTGGCAAACCTTCAGAAAAACAACCTTTTTGCTGCACATGTAAGTGGAGCTG
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTTCAGACCATCCTTTCCTACCAAATG
CAGCCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
TTTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTG
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTGATGAAAGGAT
AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTA
TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

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FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFI¹FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQM²QPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSF³FGFFLT⁴YIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

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FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCTGTTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
CCGGGGTGCGGAGCCGACATGCGCCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCAC
CTTCGCCTTGTA CTGTGCTGTCGACGCGACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGG
AGGCTGGAGGCAGGTCGCTGTGGTTCCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTTGCTCTTCTGCGGCGCCTA
CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT
TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGT
GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT
TGAGACTTTTCCCCATGACACCAACTGGTTCTTGAACCTCTCGGCCCAATTCTGAACATT
CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCATCTGTGT
GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCCTCATTAAAAAATTT
AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
CACATTGATCTGGATTTTCTGTTTGGCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
TGTGGTCCCTCTAAAGCCCCTCATTGTTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT
GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC
ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGC
AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTGCAGTAAGCCAAGATCACACCACTGCACT
CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYR
 KEHQAYVFLFLFCGAYLYKQGFaipGSSFLNVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS
 IFGKQLVVSYPDPKVALLQRKVEENRNSLFFFLFLRLFPMPNPNWFLNLSAPILNIPVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACCTGCCAGCTCAGAA
TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA
TTTATGACAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCA¹TCAGTGTGGCATG
TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
GAAGTACATGTCAGAAAATAAGGGAGTTCCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTCTGCC
AACTGCACTGGCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCCTGTTGGAGGAAGAGATTC
AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
TGGTGGCGCTGCTTTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATG
CCTCTTTAAACAAGTGCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
GTGCCGAAGACATTGTCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTGCG
ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
GGAACCGCTTTCTCAGAACTGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA
AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAAACGATGAAACTGCAAAAA

FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGGFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFV
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRCQSVAMP
IEPGDIGYVDTTTHWKVYVIARGVQPLVICDGTAFSEL

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FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTTCCGAACCTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

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FIGURE 22

CCCACGCGTCCGCCCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG
 CCACTGGTGCGCACGCTGCTAGACCGTGCCTATGAGCCGCTGGGGCTGCAGTGGGGACTGCC
 CTCCCTGCCACCCACCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA
 CACCCGAATGGCGCCACTTCATCGACAAACAGGTACAGCCAACC**ATG**TCCAGTTTCGAAATG
 GACACGTATGCTAAGAGCCACGACCTTATGTGAGGTTTCTGGAATGCCTGCTATGACATGCT
 TATGAGCAGTGGGCAGCGCGCCAGTGGGAGCGCGCCAGAGTCGTGCGGCGCTTCCAGGAGC
 TGGTGCTGGAACCTGCGCAGAGGCGGGCGCGCCTGGAGGGGCTACGCTACACGGCAGTGCTG
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCACTGGGGGGCGCTGTGGCGCCAGCT
 CGCCAGCCCATGTGGGGCCTGGGCGCTGAGGGACACTCCCATCCCCCGCTGGAAACTGTCCA
 GCGCCGAGACATATTACGCGATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTGACACCCACCGAGGAGGC
 CTCACTGCCTCTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCCACCCGAGTTGCTGCAGG
 AGGACCAGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGCAGCAGAACTG
 GATGAGCAGCGTGAGAAGCTGGTGCTGTCGGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT
 GGTCCAGGGCTGCTGGAGGTCAACACAGAAATGTATACTTCTACGATGGCAGCACTGAGC
 GCGTGGAACCCGAGGAGGGCATCGGCTATGATTTCCGGCGCCCACTGGCCAGCTGCGTGAG
 GTCCACCTGCGGCGTTTCAACCTGCGCGGTTTCACTTGGAGCTTCTTTTATCGATCAGGC
 CAACTACTTCTCAACTTCCCATGCAAGGTGGGCACGACCCAGTCTCATCTCCTAGCCAGA
 CTCCGAGACCCAGCCTGGCCCCATCCCACCCATACCCAGGTACGGAACCCAGGTGTACTCG
 TGGCTCCTGCGCCTACGGCCCCCTCTCAAGGCTACCTAAGCAGCCGCTCCCCCAGGAGAT
 GCTGCGTGCTCAGGCCTTACCCAGAAATGGGTACAGCGTGAGATATCCAACCTTCGAGTACT
 TGATGCAACTCAACACCATTTGCGGGGCGGACCTACAATGACCTGTCTCAGTACCCTGTGTTC
 CCCTGGGTCTGCAAGGACTACGTGTCCCCAACCCTGGACCTCAGCAACCCAGCCGTCTTCCG
 GGACCTGTCTAAGCCCATCGGTGTGGTGAACCCCAAGCATGCCAGCTCGTGAGGGAGAAGT
 ATGAAAGCTTTGAGGACCCAGCAGGGACCATTGACAAGTTCCACTATGGCACCCACTACTCC
 AATGCAGCAGGCGTGATGCATACCTCATCCGCGTGGAGCCCTTCACTCCCTGCGAGCCTCCA
 GCTGCAAAAGTGGCCGCTTTGACTGCTCCGACCGGCACTTCCACTCGGTGGCGGCAGCCTGGC
 AGGCACGCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATTTCTTACTTTTCT
 GACTTCCTGGAGAACCAGAACGGTTTTGACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCGATGTGGTGCTACCCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCGCC
 AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGCGGAGCCGCGGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGCAGACTCCCTGTGAGCTGCTGAAGGAGCCACATCCAACCTCGGCTCTCA
 GCTGAGGAAGCAGCCCATCGCCTTGACGCGCTGGACACTAACTCACCTAGCATCTTCAGCA
 CCTGGACGAATCAAGGCATTCTTCGACAGAGTGACTGTGAGTGCCAGTGGGCTGCTGGGCA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAGACCCC
 ACCATGGGCAGCCACAAGACGCAGCGACTGCTGAGTGGCCCGTGGGTGCCAGGCAGTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAAGCTGCTATTACGCGGTGGCCACTGGG
 ATGGCAGCCTGCGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCACGTGCATGGTGTTGGCGGCTCCTGCATCAGGGTGGTCTGTGAGTAGGCCTGGCAC
 CAAAGCCTGTGCAGGTCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT
 GAACTTGACATGGCTGTGTCTGGATCTGAGGATGGAAGTGTGATCATAACACTGTACGCCG
 CGGACAGTTTGTAGCGGCACTACGGCCTCTGGGTGCCACATTCCTGGACCTATTTTCCACC
 TGGCATTGGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGAACGTCTCTGGGGCC
 CAGGTCACCTACTCCTTGCACCTGTATTGAGTCAATGGGAAGTTGCGGGCTTCACTGCCCT
 GGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTTGTGTTGCTGGGCACCGCCAGT
 GCGCCCTGCACATCCTCCAATAAACACACTGCTCCCGGCCGCGCCTCCCTTGGCCATGAAG
 GTGGCCATCCGCAGCGTGGCCGTGACCAAGGAGCGCAGCCACGTGCTGGTGCGGCTGGAGGA
 TGGCAAGCTCATCGTGGTGCTGCGGGGCGAGCCCTCTGAGGTGCGCAGCAGCCAGTTCGCGC
 GGAAGCTGTGGCGGTCTCTGCGGGCGCATCTCCAGGTGTCTCGGGAGAGACGGAATACAAC
 CCTACTGAGGCGCGCT**TGA**ACCTGGCCAGTCCGGCTGCTCGGGCCCCGCCCCCGGAGGCCTG
 GCGGGGAGGCCCCGCCCAGAAGTCGGCGGGAACACCCCGGGGTGGGCAGCCAGGGGGTGA
 GCGGGGCCCCACCTGCCAGCTCAGGGATTGGCGGGCGATGTTACCCCTCAGGGATTGGCG
 GGCGGAAGTCCCGCCCCCTCGCCGGCTGAGGGGCGCCCTGAGGGCCAGCACTGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELTP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDYGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELEFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGR TYNDL
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSCDRQFHSVAAAWQARLESPADV KELIP
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCYTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPTMGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYLIISGRDTCMVWRL LHQGLSVGLAPKPVQVLYGHGA AVS
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFFGPFI FHLALGSEGQIVVQSSA
 WERPGAQVTYSLHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLLEDGKLIVVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
CACGGCCCACCTTGTGAACTCCTCGTGCCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCCTGGGGCTCTTC
TGGACCCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTT
CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
GCACACTCCGTTACCACACTGGGTCAATTGGCATTTGGAGCCCTCATCCTGACCCTTGTGCAG
ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
AATGCGTTCATGCTACTCATGCGAAACATTGTCAGGGTGGTTCCTGGACAAAGTCACAGA
CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCCTGTCCTTCTTTT
TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCCACCTCAACTATTAC
TGGCTGCCCATCATGACCTCCATCCTGGGGGCCTATGTCATCGCCAGCGGCTTCTTCAGCGT
TTTCGGCATGTGTGTGGACACGCTCTTCCTCTGCTTCCTGGAAGACCTGGAGCGGAACAACG
GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGGCCCTGATCCAGGACTGC
ACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCAGCTAC
TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAA
AAAGATTTTATTAAAGATATTTTGTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLGF
WTLNWWLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLLKILGKKN
EAPPDNKKRKK

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FIGURE 26

GAGTCTTGACCGCCGCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCGGT
GGCTATGTTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTT
CAGTGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGC
ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG
ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
GTGGAGCAAACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
CTTGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTTGCAGCG
CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
CACGGATCTCCTTTGAGTATGACCTCCGCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
GCGGCTCCAGGAGTTCCTTGACAGCATGGGTCTTCCCCTGAAGCAGGTGAAGCAGAAGTTCC
AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAATAAA
TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCATTTTGGGTTCAGCACAAAGTT
TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
TACCATGGCCTGGAACCTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
CTTTGCACCAACCTCGTCATCTCCAGGGGCCTTTCCTGTACTGCTCTCTCATGGAGGGCAC
TCCAGATGTCATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
AGTCCTTTGTGTGTTTCGACAAAGAACCGGCGCTGCAAACCTGCTGCCCCCTGGTGATGGCTGCC
CCCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA
TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
CTGGACGCACTTATTTCCCTCCTGTCCTAGGAAATTGATTCTTCCAGAATGACCTTCTTATT
TATGTAACCTGGCTTTTCAATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
TTTTATTAAATAAAATGCTTATTTTAGGAAA

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FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEEDDEHSGNDSGDSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
LQEF LADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNF DLSVIELKAEDRSKFL
DALISLLS

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FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAAC
 CACGAAGGGACGATACCAGAAAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTTGGCTATAGAAAAAAGAAAGGAACGAAAGAGACAGTTTTTTTTTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAACAATT
 GAGTAAAGTACGCTCCGGTCACC**ATG**GTGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTC
 CTGCTCTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC
 CAGCGGCTGCCAACGGTGTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAG
 CCTCTTCCCTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCTACATTAATATCACCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG
 GCGCCCCGTGCCAGAAGCGCTTCTTCGCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC
 GGCGAGGACTTCCAGACGCTGTCTTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCGACCGGCAGTTTGTGCTCCTCCCTGCGTGGCATCTACTTCTTCAGCCTCAATGTGC
 ACAGCTGGAATTACAAGGAGACGTACGTGCACATTATGCATAACCAGAAAGAGGGCTGTCTATC
 CTGTACGCGCAGCCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCGCGTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGCA
 ACGACTTCGACACCTACATCACCTTACGCGGCCACCTCATCAAGGCCGAGGAC**TGAG**GG
 CCTCTGGGGCACCCCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCCCGGGGACCTGGCATTCTGGGGAGA
 CCCTGCTTCTATCTTGGCTGCCATCATCCCTCCAGCCTATTTCTGCTCCTCTCTCTCTCT
 TGGACCTATTTTAAAGAGCTTGCTAACCTAAATATTCTAGAACTTTCCAGCCTCGTAGCCC
 AGCACTTCTCAAATTTGAAATGCATGCGAATCACCCGGGGTTCGTGTTAAATGCAGATTCT
 GACTCAGCAGGTCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGCTG
 ATGGGGTCAGTCTATGAACCACACTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAG
 TACTTTCTGAACATTCTGGAATCCTCCCCACATTCTAGAACTTCTCCCAACATTTTTTTTTCT
 TGAGACAGAGTCTTGCTCTGTTGCCCAGGCTAGAGTGCAGTGGTGAATCTCAGTTCAGTGC
 AACCTCTGCCTCCCGGGTCAAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTAC
 AGCGCCTGCTACCATGCCTGGCTAATTTTTGTATTTTGTAGTAGAGATGGGGTTTACCATA
 TTGGCCAGGCTGGTCTTGAACCTCCTGACTTCAGGTGACCCACCCGCTCGGCCTCTCAAAT
 GCTGGGATTACAGGTGTGAGCCACCGTGCCTGGCCAATTCCAACATTCTTAAATTCTCTCAT
 CCCTCCAGGGCTCCCGGTGCTATGTTCTCTTTACCCCTTCCCCCTCTTCTCTTGCTCAGGCC
 TGCACCACTGCAGCCACCGTTCATTTATTATTTCATTCAATTAACACTGAGCACTCACTCTGTGCT
 GGGTCCCGGGAAGGGTGAGGGGGTCAGACACAGGCCCTGCCCTGCCCTCAGTGAAGTGGCCA
 GTCCAGCCCAGGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCTCATGGGG
 GCCTGTGTTCTGGGTGTTGAGGTGCTGCTGGTCCATTACCCACTGCTCCCCAAGGCTGG
 TGGGACGGGGTCCCGGTGGCAGGGGCAGGTATCTCCTTCCCGTTCCTCATCCACCTGCCAG
 TGCTCATCGTTACAGCAAACCCAGGGGGCCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGCCCCGAAGAATGGAACCCACACCCA
 TAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAGACCTGCCCTCCTCACTGGGATCCC
 CTTCCTGCCTCCTCCCAGGGCTCTGCCAGGGCCTTGCTCAGTCCCTTCCACCAAAGTCATCT
 GAACTTCCGTTTCCCCAGGGCCTCCAGCTGCCCTCAGACACTGATGTCTGTCCCCAGGTGCT
 CTCTGCCCTCATGCCCTCTCACCGGCCAGTGCCCCGACTCTCCAGGCTTTATCAAGGTG
 CTAAGGCCCGGGTGGGCAGCTCCTCGTCTCAGAGCCCTCCTCCGGCCTGGTGCTGCCTTTAC
 AAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAAGGAGGGACCTCAGGCCTTCCGTTTCTTCTTCCAGGGTGGGGTGGCCTGGT
 GTTCCCCTAGCCTTCCAAACCCAGGTGGCCTGCCCTTCTCCCCAGAGGGAGGCGGCCCTCCG
 CCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCGGGGGGTGATCTCTGGTGCTCAC
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAAACAGGGTCTGACCAAGTGCCAGGA
 AGACCTGTGCTATAAACCACCCTGCCTGATCCTGCCCTGCCTGACCCCGCCACGCCCTGCC
 GTCCAGCATGATTAAAGAATGCTGTCTCCTCTTGAAAAA

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

C1q domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTG
 AGGCCGCGGCCTGCCCCGCCCCGGCTCCCTGCGCCGCCGCCCTCCCGGGACAGAAG**ATG**TG
 CTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGCAGG
 GCTGCCCATCCGGCTGCCAGTGCCAGCCAGCCACAGACAGTCTTCTGCACTGCCCCGCCAGGGG
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCAT
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCCTGGACCTGTCAC
 AGAACCAGATCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACTCAGCAACCTG
 GACCTGACGGCCAACAGGCTGCATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCT
 CGAGCGCCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCCGCTGCGC
 CTGCCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACAC
 CCGCATTGCCAGCTGCGGCCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCTGCGG
 CTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCCTG
 GGTGCGCGAGAGCCACGTCACTTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCCGCCA
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCCAGCCACCACC
 ACCACAGCCACAGTGCCCCACCACGAGGCCCCGTGGTGCGGGAGCCACAGCCTTGTCTTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTCCA
 CTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC
 AATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTT
 CACGGGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCCCAGCCCTACACCAGTCA
 CGCCGAGGCCACCACGGTCCCTGACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG
 AGTACACGGTCAACCAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGG
 CCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTGCGGGGAGGGCCATACACCCCCAGCCGTCCA
 CTCCAACCACGCCCCAGTCAACCAGGCCCGCGAGGGGCAACCTGCCGCTCCTCATTGCGCCCG
 CCCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGG
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGGCCCT
 GGAAGTGGAGGGAGTGAAGGTCCCCCTTGAGGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAG
 AGGCCCTGCCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTC
 CAGTCAACCCTCCACGCAAAGCCCTACAT**CTAA**GCCAGAGAGAGACAGGGCAGCTGGGGCCG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG
 GGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA
 CCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTG
 TGAAGTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG
 GGAAGATGTTTTTCAAATCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATG
 AAGGCCTTTTGTAAAGAAAAATAAAGATGAAGTGTGAAA

FIGURE 32

MCSRVP L L L L L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N
G I T M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R
R L E R L Y L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P
G I L D T A N V E A L R L A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G
N T R I A Q L R P E D L A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G
P W V R E S H V T L A S P E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S
S S L A P T W L S P T A P A T E A P S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E
G F T G L Y C E S Q M G Q G T R P S P T P V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L
T Y R N L S G P D K R L V T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A
V H S N H A P V T Q A R E G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G
P L E L E G V K V P L E P G P K A T E G G G E A L P S G S E C E V P L M G F P G P G L Q S P L H A K P Y I

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
CTTCATCATTTCATATGAGGAAATAAGTGGTAAAATCCTTGGAAATACA**AT**GAGACTCATCAG
AAACATTTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG
AAGAAAGGGAACTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG
ACCCAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTTCAACTCCAGAGTTCAGA
TTTTCAATTCTGTCTCCAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCAACAGCTGG
ATCTCAAAACCTTTGAATTCAACAAGGAGTTAAGATATTTAGATTTTGTCTAATAACAGACTG
AAGAGTGTAACTTGGTATTTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT
TGACACCATGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA
GTGGGGCAAAAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACTGTC
TTCTTAGGATTCAGAACTCTTCCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAAC
AAAAGTGCACATTGTTTTACCAATGGACACAAATTTCTGGGTTCTTTTGGGTGATGGAATCA
AGACTTCAAAAATATTAGAAAATGACAAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAA
ATGCAACGAAATCTTAGTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
TTTACTCTGGGACGACCTTTTCTTATCTTACAATTTGTTTGGCATACATCAGTGGAACTACT
TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC
TCAAATACTGTAATGAGAACTATAAAATTTGAGCATGTACATTTTTCAGAGTGTTTTACATTCA
ACAGGATAAAAATCTATTTGCTTTTGACCAAAAATGGACATAGAAAACCTGACAATATCAAATG
CACAAATGCCACACATGCTTTTCCCGAATTATCCTACGAAATTCGAATATTTAAATTTTGGC
AATAATATCTTAAACAGACGAGTTGTTTAAAAGAACTATCCAAGTGCCTCACTTGAAAACCTCT
CATTTTGAATGGCAATAAACTGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACAACACAC
CCTTGGAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAAATGATGAAAATTTGCTCA
TGGCCAGAACTGTGGTCAATATGAATCTGTGCATACAATAAATTTGTCTGATTCTGTCTTCAG
GTGCTTGCCCCAAAAGTATTCAAATACTTGACCTAAATAATAACCAATCCAACTGTACCTA
AAGAGACTATTCATCTGATGGCCTTACGAGAACTAAATATTGCATTTAATTTTCTAACTGAT
CTCCCTGGATGCAGTCATTTTCAGTAGACTTTTCAGTTCTGAACATTGAAATGAACCTTCATTCT
CAGCCCATCTCTGATTTTGTTCAGAGCTGCCAGGAAGTTAAACTCTAAATGCGGGAAGAA
ATCCATTCCGGTGTACCTGTGAATTAATAAATTTTCATTCAGCTTGAAACATATTCAGAGGTC
ATGATGGTTGGATGGTCAGATTTCATACACCTGTGAATACCCTTTAAACCTAAGGGGAAGTAG
GTTAAAAGACGTTTCATCTCCACGAATTATCTTGCAACACAGCTCTGTTGATTGTACCATTTG
TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCCC
TGGTATCTCAGGATGTCTAGTCAATGCACACAAACATGGCACAGGGTTAGGAAAACAACCCA
AGAACAACCTCAAGAGAAATGTCCGATTCCACGCATTTATTTTCATACAGTGAACATGATTCTC
TGTGGGTGAAGAATGAATTGATCCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGATTTGC
CTTTATGAAAGCTACTTTGACCCTGGCAAAAGCATTAGTGAAAATATTGTAAGCTTCATTGA
GAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCAACTTTGTCCAGAATGAGTGGTGCCATT
ATGAATTTCTACTTTTGGCCACCACAATCTCTTCCATGAAAATTTCTGATCATATAATTTCTTATC
TTACTGGAACCCATTCCATTCTATTGCATTCCCACCAGGTATCATAAACTGAAAGCTCTCCT
GGAAAAAAAAGCATACTTGAATGGCCCAAGGATAGGCGTAAATGTGGGCTTTTCTGGGGCAA
ACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCAGAGAAATGTATGAACTGCAGACA
TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTGTCT
ATAAAATCCCACAGTCCTTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTGATA
CAACCTTTATGATGGCAATTTGACAATATTTATTAAATAAAAAATGGTTATTCCTTTCATA
TCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACACCTTCACAAGTTTATAAGG
GCTTATGGAAAAAGGTGTTTCATCCCAGGATTGTTTATAATCATGAAAAATGTGGCCAGGTGC
AGTGGCTCACTCTTGAATCCCAGCACTATGGGAGGCCAAGGTGGGTGACCCACGAGGTCAA
GAGATGGAGACCATCTGGCCAAACATGGTGAAACCTGTCTCTACTAAAAATACAAAAATTA
GCTGGGCGTGATGGTGCACGCCTGTAGTCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCG
CTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTGCACTCCAGCCTGGT
GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAATGGAAAAACATCC
TCATGGCCACAAAATAAGGTCTAATTCATAAATATAGTACATTAATGTAATATAATATTA
CATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCTGGTATGGAAAAAATATTAATAT
GTTATAAACTATTAGGTTGGTGCAAACTAATTGTGGTTTTTGGCATTGAAATGGCATTGAA
ATAAAAGTGTAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGTCTGGGAGGTTGGA
TTACAGGGAGCATTTGATTTCTATGTTGTGATTTCTATAATGTTTGAATTGTTTAGAATGA
ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

FIGURE 34

MRLIRNIYIFCSIIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLLQHKNDENC SWPETVVNMNLSYNKLS
DSVFRCLPKSIQILD LNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGC SHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHNNLFHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

GGGGGCTTCTTGGGCTTGGCTGCTTGGAAACACCTGCCTCCAAGGACCGGCCTCGGAGGGGTGCGCGGAAAGG
GAGGGAAGTAAGGAAGGGCGGGGCCCGCCCCCTGCGCCCGCCCCGCGCCTCTGCGCGCCCTGTCCGCCCGGGC
CCAGCCCAGCCCAGCCCCGCGGGCCGGTACACGCGCAGCCAGCCGGCCGCCTCCCGCGCCCAAGCGCGCCGCT
CTGCTGTGCCCTGCGCCCTTGGCCCCGCGCCAGCTTCTGCGCCCCGAGCCCGCCCCGGCGCCCCCGGTGACCGTGA
CCCTGCCCTGGGCGCGGGGCGGAGCAGGCATGTCGCCGCCGGGGACCGCTACCCCAAGCGCTGGCCCTGGTGCT
CTGGCAGTGACCCCTGGCCGGGGTCGGAGCCCCAGGGCGCAGCCCTCGAGGACCTGATTATTACGGGCGAGGAGAT
CTGGAGCCGGGAGCCCTACTACGCGCCCGGAGGCCGAGCTCGAGACCTTCTCTCCGCCGCTGCCTGCGGGGC
CCGGGGAGGAGATGGGAGCGGCGCCCCGAGGAGCCAGGCCGCCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCC
AAGAGGGAGAAGTCGGCTCCGGAGCCGCTCCACCAGGTAAACACAGCAACAAAAAGTTATGAGAACCAAGAG
CTCTGAGAAGGCTGCCAACGATGATCACAGTGTCCGTGTGGCCCGTGAAGATGTGAGAGAGAGTTGCCACCTC
TTGGTCTGGAACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCCTGGGGCA
CATCGAGGGAGACTCAACATCCAGGCGGGCATTAATGAAATGATTTTTATGACGGAGCGTGGTGCGCGGGAAG
AAATGACCTCCAGCAGTGGATTGAATGGATGCTCGGCCCTGACCAGTACTGGTGTCTACTCACTCAAGGGA
GGAACCTCCTCTGGCTGAGTGACTGGGTGACATCCTATAAGGTCTGCTGAGCAATGACAGCCACACGTGGGT
ACTGTTAAGAATGGATCTGGAGACATGATATTTGAGGGAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCT
ACCCGTCCCCATGGTGGCCCGCTACATCCGCATAAACCCCTCAGTCCCTGGTTTGATAATGGGAGCATCTGCATGA
GAATGGAGATCCTGGGCTGCCACTGCCAGATCCTAATAATTATTATCACCGCCGGAACGAGATGACCACCCT
GATGACCTGGATTTTTAAGCACCACAATATAAGGAAATGCGCCAGTTGATGAAAGTTGTGAATGAAATGTCTC
CAATATCACCAGAATTTACAACATTGAAAAAGCCACAGGCCCTGAAGCTGATGTGCTGGAGATCTCAGATC
ACCTGGGGAGCATTAAGTCGGTGAGCCCCGAGTTCCACTACATCGCGGGGGCCACGGCAATGAGGTGCTGGGC
CGGGAGCTGCTGCTGCTGCTGGTGCAGTTCGTGTGTGAGGAGTACTTGGCCCGGAATGCGCGCATCGTCCACCT
GGTGGAGGAGACGCGGATTACGTCCTCCCTCCCTCAACCCCGATGGCTACGAGAAGGCCTACGAAGGGGGCT
CGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGACCCACGATGGAATTGACATCAACAACAACCTTTCTGATTTA
AACACGCTGCTCTGGGAGGCAGAGGATCGACGAATGTCCCCAGGAAAGTTCCCAATCACTATATGCAATCCC
TGAGTGGTTTCTCTGGGAAATGCCACGGTGGCTGCCAGACGAGCAGTCAATAGCCTGGATGGAAAAAATCC
CTTTTGTGCTGGGCGGCAACCTGCGAGGGCGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGCGGTCCCC
TGGAAGACGCAGGAACACACCCCCACCCCGATGACCACGTGTTCCGCTGGCTGGCTACTCCTATGCCTCCAC
ACACCGCCTCATGACAGACGCCCCGAGGAGGGTGTGCCACACGGAGGACTTCCAGAAGGAGGAGGGCAGTGTCA
ATGGGGCCTCCTGGCACACCGTCGCTGGAAGTCTGAACGATTTTCAGTACCTTATACAAACTGCTTCGAATG
TCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGTCCCCGAGGAGTGGGAGATAACCGGGAATC
TCTGATCGTGTTCTGAGCAGGTTTCATCGTGGCATTAAGGCTTGGTGAGAGATTACATGGAAAAGGAATCC
CAACGCCATTATCTCCGTAGAAGCATTAACCATGACATCCGAACAGCCAACGATGGGGATTACTGGCGCCTC
CTGAACCCCTGGAGAGTATGTGGTTCACAGCAAAGGCCGAAGGTTTCTGTCATCCCAAGAAGTGTATGGTTGG
CTATGACATGGGGGCCACAAGGTGTGACTTCACACTTAGCAAAACCAACATGGCCAGGATCCGAGAGATCATGG
AGAAGTTTGGGAAGCAGCCCGTCAGCCTGCCAGCCAGGCGGCTGAAGCTGCGGGGGCGGAAGAGACGACGCT
GGGTGACCCCTCCTGGGCGCTTGAGACTCGTCTGGGACCCATGCAAAATTAACCAACCTGGTAGAGCTCCATG
TGGACTCACTCACTGTTGTTCTCTGTAATTCAAGAAGTGCTTGAAGAGAGGGTGCATTGTGAGGCAGGTCC
CAAAAGGGAAGGCTGGAGCTGAGGCTGAGGCTGTTTTCTTTTCTTTGTTTCCCATTTATCCAAATAACTTGGACAGAGCA
GCAGAGAAAAGCTGATGGGAGTGAGAGAACTCAGCAAGCCAACCTGGGAATCAGAGAGAGAAGGAGAAGGAGGG
GAGCCTGTCCGTTTACAGCCTCTGGCTGCATAGAAAAGGATTCTGGTGCTTCCCTGTTTGGTGGCAGCAAGG
GTTCCACGTGCATTTGCAATTTGCACAGCTAAAATTGCAGCATTTTCCCAGCTGGGCTGTCCCAATGTTACCA
TTTGAGATGCTCCCAGGCGTCTTAAGAGAATCCACCCTCTCTGGCCCTGGGACATTGCAAGCTGCTACAAATA
ATTCTGTGTTCTTTTGACATAGCGTCATTGCCAAGTGACATCAGTGAGCCCTTGAACTCTGTTAGTCTCCT
TTTTCAACAAGAGGTGTGTTTCAGAAAAGGAGAGAGGCTGAGATCATTCAGGAGTTTGTGGGCAGCAAGCA
TGGAGCTTCTTGCACAAATTCTGGGTCCATAAACAACCCCCAAAGTCCCTGCTGATCCAGTAGCCCTGGAGGTT
CCCCAGGTAGGGAGAGCCAGAGGTGCCAGCCTTCCCTGAAGGGCCAGAAAATTTAGCCTGGATCTCCTCTTTTAC
CTGCTAGGACTGGAAAGAGCCAGAAGTGGGGTGGCCCTGAAGCCCTCTCTGCTTGGAGTATTGCCCCCTGTGTG
GAATTGAGTGCTCATGGGTGGCCCTCATATCAGCCTGGGAGTTATTTTGATATGTAGAATGCCAGCTATCCCA
GATTAGGCTAAATGATGATAAACCCTCTTAGGATTATCTGGAGCATGATGTTGGGAAGAATTATTGAATTAT
CTTGAAGAAAAAGTATGTCTCACTTTTTGTTAATGTTGCTGCCTCATTGACCTGGGAAAAATGAAAAAAA
AATAAAGCAATGGTAAGACCCTTAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPPLP
AGPGEEWERRPQEPRPPKRATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNKSGDMI F
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG
SELGGWSLGRWTHDGIDINNNFDPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYS YAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLGRKRQRG

FIGURE 37

CTAAGAGGACAAG**ATG**AGGCCCCGGCCTCTCATTTCTCCTAGCCCTTCTGTTCTTCCCTTGGCCAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAATTCCCAGCCCCGGCTTCAGCTCTTTCCCAGGTGTTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTCGGGCTCCAGCTCCAGCCGACGCTTAGGCAGCGGAGGTTCTGTGTCCCAGTTGTT
 TTCCAATTTACCCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGCTCTGTTTCCCTGCCAGACACCACCTTTC
 CCGTGGACAGAGTGGAACGCTTGAATTACAGCTCATGTTCTTTCTCAGAAGTTTGAGAAAAGAACTTTCTAAA
 GTGAGGGAATATGTCCAATTAATTAGTGTGTATGAAAAGAACTGTTAAACCTAACTGTCCGAATTGACATCAT
 GGAGAAGGATACCATTTCTTACACTGAAGTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC
 TGGTCATACAGCTGAAGGAGAGTTTTGGTGGGAAGCTCAGAAAATTGTTGACCAGCTGGAGGTGGAGATAAGAAAT
 ATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAAACAATGTCCTTGCCATTGCGCGAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAAACACCCCTGTCGTCCACCTCCTCCCACTC
 CAGGGAGCTGTGGTTCATGGTGTGGTGAACATCAGCAAACCGTCTGTGGTTTCAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTCCCCAGCATCCAAACAAAGGACTGTATTGGGTGGCGCC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTTGCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAAC
 TGCTGCCTATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTTATTTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAAACTCAATGACACCACACTT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCTTCATGGTATGTGGGGTCT
 GTATGCCACCCGTACTATGAACACCAGAACAGAAGAGATTTTTTACTATTATGACACAAACACAGGGAAAGAGG
 GCAAACATAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACATAACCCTTTTGACCAGAAA
 CTTTATGTCTATAACGATGGTTACCTTCTGAATTATGATCTTTCTGTCTTGCAAGCCCCAG**TAA**GCTGTTTA
 GGAGTTAGGGTGAAAGAGAAAAATGTTTGTGAAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAAAGTGTGTTTCAATTTTGCAGCAATGTTTGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCT
 TGATTTGGTGAGTTCTCTTGGGAATCATCTGCCTCTTCAGGCGCATTTTGCAATAAAGTCTGTCTAGGGTGGGA
 TTGTCAGAGGTCTAGGGGCACTGTGGGCCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA
 GGAATTAAGGAACCTAAACTCAGTATGGCGTCTAGGGATTCTTTGTACAGGAAATATTGCCAATGACTAGTC
 CTCATCCATGTAGCACCACCTAATTCTTCCATGCCTGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAATATCT
 GGAGCTCCTCGAGGGACCAATCTCCAACCTTTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAAGTGCTGAGTTTTATGGAGAGAGGCCTTTTT
 ATGCATTAAATTGTACATGGCAATAAATCCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTTCTTTCTCTC
 ATTTGTCCACCTTACTAAAAGTCAGTAGAATCTTCTACCTCATAACTTCCTTCCAAAGGCAGCTCAGAAGATTAG
 CTATGGAACCTGATCTAAGATTAGAAAAATTAATTTCTTTAATTTTATTATGGACTTTTATTTACATGACTCTA
 AGACTATAAGAAAATCTGATGGCAGTGACAAAGTGCTAGCATTTATTGTTATCTAATAAAGACCTTGGAGCATA
 TGTGCAACTTATGAGTGTATCAGTTGTTGCATGTAATTTTTGCCTTTGTTTAAGCCTGGAACCTGTAAGAAAAT
 GAAAATTTAATTTTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT
 TGGAAACCTTGCTGGTGTATGTGATGTGCTTCTGTGCTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT
 TCCTTTGATGTTCAAGTCCTAGTCTATAGGATTGGCAGTTTAAATGCTTTACTCCCCCTTTTAAATAAATGAT
 TAAATGTGCTTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA

MRPGLSFL LALLFFLGQAAGDLGDVGPPIPSPGFS SFPGV DSSSSFS SSSSRSGSSSSRSLGS
GGSVS QLF SNFTG SVDDR GTCQCSVSLPDTTFPVDR VERLEFTAHVLSQKF EKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNM TLLVEKLETLDKNNVLAIRREIVAL KTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVVNISKPSV VQLNWRGFSYLYGAWGRDYS PQHPNKG LYWVAPLNTDGRLL EYYRLYNTLD
DLLLYINARELRITYGQSGTAVYNNNMYVNMYNTGNIARVNLTTNTIAVTQTLPNAAYNRR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTTLQVLNTWYTKQYKPSASNAF
MVCGLVYATR TMNTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCCTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

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FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTGTGACGTTGTGGAG**ATG**GGGAGCGTCCTGGGGCTGTGCTCCATGGCGAGCT
 GGATACCATGTTTGTGTGGAAAGTGCCCCGTGTTGCTATGCCGATGCTGTCCTAGTGGAAC
 AACTCCACTGTAAGTAGATTGATCTATGCACTTTTCTTGCTTGTTGGAGTATGTGTAGCTTG
 TGTAATGTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCCCTGGATTTTGTGAGAATG
 AGAAAGGTGTTGTCCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GGTTTGGCTATGTTCTATCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
 TCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTA
 TTATTGGGGCATTCTTCATTCCAGAAGGAACTTTTACAACCTGTGTGGTTTTATGTAGGCATG
 GCAGGTGCCTTTTGTTCATCCTCATACAACCTAGTCTTACTTATTGATTTTGCACATTCATG
 GAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCAGCCTTGT
 TATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTCTTGTCTAC
 TACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGCGTTCATCAGTGTCAACATGCTCCTCTG
 CGTTGGTGCTTCTGTAATGTCTATACTGCCAAAAATCCAAGAATCACAACCAAGATCTGGTT
 TGTTACAGTCTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT
 GAACCAGAAACAAATTGCAACCCCAAGTCTACTAAGCATAATTGGCTACAATAACAAGCAC
 TGTCCCAAAGGAAGGGCAGTCAGTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTAATTC
 TCTTTTGTGTGTGTTATTTTATTCAGCATCCGCTACTTCAAACAATAGTCAGGTTAATAAAA
 CTGACTCTAACAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGGATC
 ACTGGAGGATGGGGACGATGTTACCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA
 GTTATTCCTTCTTTCACCTCATGCTTTTCTGGCTTCACTTTATATCATGATGACCCCTTACC
 AACTGGTCCAGGTATGAACCCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTCTGGGTGAA
 AATCTCTTCCAGTTGGATTGGCATCGTGCTGTATGTTTGGACACTCGTGGCACCCTTGTTC
 TTACAAATCGTGATTTTGA**CTG**AGTGAGACTTCTAGCATGAAAGTCCACTTTGATTATTGC
 TTATTTGAAAACAGTATTCCCAACTTTTGTAAAGTTGTGTATGTTTTTGTCTCCCATGTAAC
 TTCTCCAGTGTTCTGGCATGAATTAGATTTTACTGCTTGTCATTTTGTTATTTTCTTACCAA
 GTGCATTGATATGTGAAGTAGAATGAATTGCAGAGGAAAGTTTTATGAATATGGTGATGAGT
 TAGTAAAAGTGCCCATTTATTTGGCTTATTCTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA
 ACAAAATTTGTTTGACTATTTTAAAAATTATATTAGACCTTAAGCTGTTTTAGCAAGCATTAAA
 GCAAATGTATGGCTGCCTTTTGAATATTTGATGTGTTGCCTGGCAGGATACTGCAAAGAAC
 ATGGTTTTATTTTAAAAATTTATAAACCAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGGTTTTTACCCTTGATACGGAATTTACACAGGTAGGGAGTGTTTAGTGGACAATAGTGTAGG
 TTATGGATGGAGGTGTCGGTACTAAATTTGAATAACGAGTAAATAATCTTACTTGGGTAGAGA
 TGGCCTTTGCCAACAAAGTGAAGTGTGTTTAACTCATGAAGTATGGGTTCAGT
 GGAAATGTTTGAAGTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTTAGA
 AGGAAGTGTTTTGAAAGTCACTTTGAAAGTTAGTTTTGGGCCAGCACGGTAGCTCACCCCTT
 GGAATCCCAGCACTTTGGGAGCTTAAGTGGGTAGATTACTTTGAGCCCAGGAATTCAGACCA
 GCTTGGCACATGTTGAACCTGTTCTATAAAAAATAATCTGGCTTTGAGCATATGCCTGTGGTC
 CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCAGAGCCAAAGGTTGCAGTGAGCAAGTCA
 CGTCACTGCACTCTAGCTGGCACAGAGTAAGCCAAAAAATATATATATATTGAAATCAAGG
 AGGCAAAATTTTGAAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGTACTTAT
 ATAAAACTAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATA
 GCTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAATAATAGCATTCTCTCTGACATTTAA
 AAATAATTTCTATTCAAATACATGCATATTGATTTACACCTCATACTGTGATAATTAATGT
 GATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTCAGAAGAATGATGGAATGTTTT
 AGAATAAACTCCTGCTTATAGTATACTACACAGTTCAAAGATGTTTTAAATGCTTTTGTAT
 TTAAGAGTTTGTATTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTACAATT
 TCTTCTTTAAAAATATTTATTAATGTGAATGGAATATAACAATTCAGCTTAATCCCCAACCC
 TTATTCTGTGTGTAGACATTGTATTCCACAATTTTGAATGGCTGTGTTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNII VGYKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDSTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI
VLYVWTLVAPLVLTNRDFD

CGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATAACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCCTAGTGGAACAANTCCACTGTAAGTAGATTGATCTA
TGCACTTTTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATAACCAGGAATGGAAG
AACAACTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNTATGCCGATGCTGTCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

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FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCCTAGTGGAAACAACCTCCACTGTAACTAGATTGATCTATGCACTT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTGTAACCTGGATTGATCTATGCACTTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAACTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

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FIGURE 46

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCTGCGATTGAGCTGCGGGTTCGCGGCCGGCGCGGCTCTCCAAT
GGCAAATGTGTGTGGCTGGAGGCGAGCGCGAGGCTTTTCGGCAAAGGCAGTCGAGTGTTCGAGACCGGGGCGAG
TCCTGTGAAAGCAGATAAAAAGAAAACATTTATTAACGTGTCATTACGAGGGGAGCGCCCGGGGCTGTGCG
ACTCCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGAAAGCGGAAAAGAGGCAGATTCAC
GTCGTTTCCAGCCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGATTTATAGCGATGCC
CCCTGGTTTTGTGTGTTACGCACACACACGTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTCC
TGGGCGAATCCCACATCTGTTTCACTCTCCGCCGAGGGCGAGCAGGAGCGAGAGTGTGTGCAATCTGCGAGTG
AAGAGGGACGAGGAAAAGAAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAGAACACCAGAT
CAGCAAAAAAGAAAGATGGGGCCCCCGAGCCTCGTGCTGTGCTTGTGTCCGCAACTGTGTTCTCCCTGCTGGG
TGGAAGCTCGGCCCTTCTGTGCGCACCACCGCCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCCA
ACATCATCTCTGGTGTGACGGACGACCAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCCGGCGC
ATCATGGAGCAGGGCGGGGCGCACTTCATCAACGCCTTCGTGACCACACCCATGTGCTGCCCTCAGCTCCTC
CATCCTCACTGGCAAGTACGTCCACAACCACAACACCTACACCAACAATGAGAACTGCTCCTCGCCCTCCTGGC
AGGCACAGCAGGAGCGGCACCTTTGCCGTGTACCTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAG
TATCTTAATGAATACAACGGCTCCTACGTGCCACCCGGCTGGAAGGAGTGGGTGCGACTCCTTAAAAACTCCCCG
CTTTTATAACTACAGCTGTGTGCGAACGGGGTGAAAGAGAAGCACGGCTCCGACTACTCCAAGGATTACCTCA
CAGACCTCATACCAATGACAGCGTGAGCTTCTTCCGCACGTCCAAGAAGATGTACCCGCACAGGCCAGTCTC
ATGGTCATCAGCCATGCAGCCCCCACGGCCCTGAGGATTAGCCCCACAATATTCACGCCTCTTCCCAAACGC
ATCTCAGCACATCAGCCGAGCTACAACACGCGCCCAACCCGGACAAACACTGGATCATGCGCTACACGGGGC
CCATGAAGCCCATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTGCAGACCCCTCATGTGCTGGAC
GACTCCATGGAGACGATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACGTACATCGTATACACCGC
CGACCACGGTTACCACATCGGCCAGTTTGGCCTGGTGAAAGGGAATCCATGCCATATGAGTTTGACATCAGGG
TCCCGTTCTACGTGAGGGGCCCCAACGTGGAAGCCGGCTGTCTGAATCCCCACATCGTCTCAACATTGACCTG
GCCCCACCATCCTGGACATTGCAGGCCTGGACATACCTGCGGATATGGACGGGAATCCATCCTCAAGCTGCT
GGACACGGAGCGGCCGGTGAATCGGTTTCACTTGAAAAAGAAGATGAGGGTCTGGCGGGACTCCTTCTTGGTGG
AGAGAGGCAAGCTGTACACAAGAGAGACAATGACAAGTGGACGCCAGGAGGAGAACTTTCTGCCAAAGTAC
CAGCGTGTGAAGGACCTGTGTGAGCGTGTGAGTACCAGCGGCGTGTGAGCAGCTGGGACAGAAGTGGCAGTG
TGTGGAGGACGCCACGGGGAAGCTGAAGCTGCATAAGTGCAAGGGCCCCATGCGGCTGGGCGGCAGCAGAGCCC
TCTCCAACCTCGTGCCCAAGTACTACGGGCAGGGCAGCGAGGCCTGCACCTGTGACAGCGGGGACTACAAGCTC
AGCCTGGCCGGACGCCGGAATACTCTTCAAGAAGAAGTACAAGGCCAGCTATGTCCGCAGTCGCTCCATCCG
CTCAGTGGCCATCGAGGTGGACGGCAGGGTGTACCACGTAGGCCTGGGTGATGCCGCCAGCCCCGAAACCTCA
CCAAGCGGCACTGGCCAGGGCCCCCTGAGGACCAAGATGACAAGGATGGTGGGACTTCAGTGGCACTGGAGGC
CTTCCCGACTACTCAGCCGCCAACCCCATTAAGTGACACATCGGTGCTACATCCTAGAGAACGACACAGTCCA
GTGTGACCTGGACCTGTACAAGTCCCTGCAGGCCTGGAAGACCACAAGCTGCACATCGACCACGAGATTGAAA
CCCTGCAGAACAAATTAAGAACCTGAGGGAAGTCCGAGGTACCTGAAGAAAAAGCGGCCAGAAGAAATGTGAC
TGTCACAAAATCAGCTACCACACCCAGCACAAAGGCCGCCCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTCAG
GAAGGGCCTGCAAGAGAAGGACAAGGTGTGGCTGTTGCGGGAGCAGAAGCGCAAGAAGAAACTCCGCAAGCTGC
TCAAGCGCCTGCAGAACAACGACACGTGCAGCATGCCAGGCCTCACGTGCTTCACCCAGACAACCAGCACTGG
CAGACGGCGCCTTTCTGGACACTGGGGCCTTTCTGTGCTGCACCAGCGCCAACAATAACACGTACTGGTGCAT
GAGGACCATCAATGAGACTCACAATTTCTCTTCTGTGAATTTGCAACTGGCTTCTAGAGTACTTTGATCTCA
ACACAGACCCCTACCAGCTGATGAATGCAGTGAACACACTGGACAGGGATGTCTCAACCAGCTACACGTACAG
CTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGGACTCGAAACATGGACCTGGATGGAGG
AAGCTATGAGCAATACAGGCAGTTTCAGCGCTCGAAAGTGGCCAGAAATGAAGAGACCTTCTTCCAAATCACTGG
GACAACCTGTGGGAAGGCTGGGAAGGTTAAAGAAAACAACAGAGGTGGACCTCCAAAACATAGAGGCATCACCTGA
CTGCACAGGCAATGAAAAACCATGTGGGTGATTTCCAGCAGACCTGTGCTATTGGCCAGGAGGCCTGAGAAAGC
AAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCAGCAGGAGCAGAGATAACTTCAGGAAGTCC
ATTTTTGCCCTGCTTTTGGATTATACCTCACCAGCTGCACAAAATGCATTTTTTCGTATCAAAAAGTC
ACCACTAACCTCCCCCAGAAGCTCACAAAGGAAAACGGAGAGAGCGAGCGAGAGAGATTTCTTGGAAATTTCT
TCCAAGGGCGAAAGTCATTGGAATTTTAAATCATAGGGGAAAAGCAGTCTGTTCTAAATCCTCTTATTCTT
TTGGTTTGTACAAAGAAGGAACATAAGAAGCAGGACAGGCAAGCTGGAGAGGCTGAAACAGTGCAGAGACG
TTTGACAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACTATAAACCCCTGGTTGCCTCTGAAGAAA
CTGCCTTCATTGTATATATGTGACTATTTACATGTAATCAACATGGGAACCTTTTAGGGGAACCTAATAAGAAAT
CCCAATTTTCAGGAGTGGTGGTGTCAATAACGCTCTGTGGCCAGTGTAAAGAAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTPMCPSRSSILTGYVHNHNTYTNNECSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMPHRPVL MVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
AGLDIPADM DGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDL CQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKY
YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSV AIEVDGRVYHVGLGDAAQ
PRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSL
HPFRKGLQE KDKVWLLREQKRKKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNNTY WCMRTINETHNFLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCCTGCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGGCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA
CGCTCGCTTGAGGCTGCTGTCGCCGGTGCCTGTGGACAGCAGCTGCCCCTGCCCTCCCATCTG
TCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTAATATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTTCATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 49

MLGLLGSTALVGWITGAAVAVLLLLLLLLLATCLEFHGRQDCDVERNRTAAGGNRVRRRAQPWPFR
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

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FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
CTACTGGGCCTGATTGGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTCACCCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCTACTGAGAGC
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCCATCCTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
AGATCTACCAGGAAGACCAGATCCATTTTCTGTGCCCACTGGCACGGCAGGGAGACTTCTAT
GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACCTGGGGCGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
GGAGCTGGACTTGAGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAG**TAA**CCC
ATGGCCTGCACCCTCCTGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCT
CCAGCCCTCTTCCTCCTTCCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGC
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA
GGGACTATTTTCTGCACCAGCCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTTTCAGACTC
ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTTCACCTGGAAAAAAA
AAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPCLRSLAVYYDNPHMVPPDKCRCAVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATTRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCT
GCCCCGCGCCCAGTC**ATG**ACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA
GACACGCTTCACATACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAATACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

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FIGURE 53

MTLRPSLLPLHLLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFCDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNSKKK

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FIGURE 54

CCCGGGAACGTGTTTCCTGGCTGCCGCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGC
CCCGCGCCCAGTCATGACCCTGCGCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTTAAAAAACTTAAAA

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAATCGGGGGAG
TGAGGCGGGCCGGCGGGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
ACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
GTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG
TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
TTCCACAGCACAACAGCCCTGCATGGGTTTGTGTTGTTTTTTACTGCTCACTCCCAACCTT
TTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACTTGATTAACCTT
ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
TGTA AAAAATAAAAAGAAATTACAAAAGAAATTATGGATTTGTCAATGTAAGTATTTGTCATA
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
CTCTTCTGTGTCAAATGTTAAATGAAATATAACATTTTTTTAGTTTTTTAAATATTCCGTGG
TCAAAATTCTTCCTCACTATAATTGGTATTTACTTTTACCAAAAATTCTGTGAACATGTAAT
GTA ACTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT
CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
CACATCCACCACTG

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FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTE DLWQ

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FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGGGCGGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTTGGAGGGCTGGTTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

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FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATAACCATGCCTGTGGTGTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

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FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGGTTCCGGGAACCATTCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

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FIGURE 63

CGACGCCGGCGTG**ATG**TGGCTTCCGCTGGTGTCTCCTGGCTGTGCTGCTGCTGGCCGTCC
TCTGCAAAGTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAACGGCCCCCAGCGCCCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGC
TTTTTTCAGCCAACCAAGTGCCGGAGAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG
GCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCCTGGTGTGGAACAACAT
ACCAAGGCAGGGGGCTGCTGTCTACCTTTGGAAAGAATGGCCTTGAATTTGACACAGGAAT
CCATTACATTGGGCGTATGGAAGAGGGCAGCATTGGCCGTTTTATCTTGGACCAGATCACTG
AAGGCGAGCTGGACTGGGCTCCCCCTGTCTCTCCTTTTGACATCATGGTACTGGAAGGGCCC
AATGGCCGAAAGGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATTCAGGGCCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA
GTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCCATTGCCCGTGGTTTCAGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTTCTCTCCATTCTTCAAGCATCCACCCAGAGCCTGCTGA
GGTCTGTGAGCAGCTGGGGGCTCCTGTAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA
CTTACGGTGTACCCCCAACACAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTAC
ATGAAAGGAGGCTTTTATCCCCGAGGGGGTTCCAGTGAAATTGCCTTCCACACCATCCCTGT
GATTTCAGCGGGCTGGGGGCGCTGTCTCACAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
CAGCTGGGAAAGCCTGTGGTGTGAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTATTGC
CCCATCGTGGTCTCCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC
CCGCTGCCTGCCAGGTGTGAAGCAGCAACTGGGGACGGTGCGGCCCCGGCTTAGGCATGACCT
CTGTTTTTCATCTGCCTGCGAGGCACCAAGGAAGACCTGCATCTGCCGTCCACCAACTACTAT
GTTTACTATGACACGGACATGGACCAGGCGATGGAGCGCTACGTCTCCATGCCCAGGGAAGA
GGCTGCGGAACACATCCCTCTTCTCTTCTCGCTTTCCCATCAGCCAAAGATCCGACCTGGG
AGGACCGATTCCCAGGCCGCTCCACCATGATCATGCTCATACCCACTGCCTACGAGTGGTTT
GAGGAGTGGCAGGCGGAGCTGAAGGGAAGCGGGGCAGTACTATGAGACCTTCAAAAACCTC
CTTTGTGGAAGCCTCTATGTGAGTGGTCTGAAACTGTTCCACAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTCACCACCAAGTCTATCTGGCTGCTCCCCGAGGTGCC
TGCTACGGGGCTGACCATGACCTGGGCCGCTGCACCCTTGTGTGATGGCCTCCTTGAGGGC
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTACCTGTGGACTGGTCTG
GGGCCCTGCAAGGTGCCCTGCTGTGTCAGCAGCGCCATCCTGAAGCGGAACCTGTACTCAGAC
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAAT**TAG**TTCCATCAGGGAGG
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
CATTAGTTCCTTGACAGTATAAAGCACTCTAATTTGGTTCTGATGCCTGAAGAGAGGCCTAG
TTTAAATCACAAATCCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG
TCTCATGACGAGCGGCGCTCTGCATCCCTCACCCATGCCTCCTAACTCAGTGATCAAAGCGA
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTGCTCAGCTCAACCTGGTGGGTTTCACTC
TGTCTGAGGCTTCTGCTCTCATTCAATTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG
GAAAAGGGAGACTAATGAGGCTTAACCTCAAAACCTGGGCGTGGTTTTGGTTGCCATTCCATA
GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCAGTGGCTCTTTCAGGGGACAGGAAT
GCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGCATGTGAGATGATCATATCCAATTCATATGGAAGTCCCGGGTCTGTCTTCTTATCA
TCGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCTCAATCAAGC
CTTATCCACCAAATACACAGGGAAGGGTGATGCAGGGAAGGGTGACATCAGGAGTCAGGGCA
TGGACTGGTAAGATGAATACTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCCAGCCAAGGG
CACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGAAGTCACATCAGAAAAGGGA
AAGCCACGGAATGTGTGTGAAGCCCAGAAATGGCATTTCAGTTAATTAGCACATGTGAGGG
TTAGACAGGTAGGTGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGTCTTTG
GTATCAGACATACGAAAGGTCTCTTTGTAGTTTCGTGTTAATGTAACATTAATAAATTTATTG
ATTCCATTGCTTTAAAAA

FIGURE 64

MWLPLVLLLLAVLLLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDKEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIIDKYIKLVKVVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLTkATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLENTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYYDTMDQAMERYVSMPREEAAEH
IPLLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAELKGKRGSDYETFKNSFVEA
SMSVVLKLFQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

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95	11	off		95	11	off	
96	12	off		96	12	off	
97	13	off		97	13	off	
98	14	off		98	14	off	
99	15	off		99	15	off	
100	16	off		100	16	off	
101	17	off		101	17	off	
102	18	off		102	18	off	
103	19	off		103	19	off	
104	20	off		104	20	off	
105	21	off		105	21	off	
106	22	off		106	22	off	
107	23	off		107	23	off	
108	24	off		108	24	off	
109	25	off		109	25	off	
110	26	off		110	26	off	
111	27	off		111	27	off	
112	28	off		112	28	off	
113	29	off		113	29	off	
114	30	off		114	30	off	
115	31	off		115	31	off	
116	32	off		116	32	off	
117	33	off		117	33	off	
118	34	off		118	34	off	
119	35	off		119	35	off	
120	36	off		120	36	off	
121	37	off		121	37	off	
122	38	off		122	38	off	
123	39	off		123	39	off	
124	40	off		124	40	off	
125	41	off		125	41	off	
126	42	off		126	42	off	
127	43	off		127	43	off	
128	44	off		128	44	off	
129	45	off		129	45	off	
130	46	off		130	46	off	
131	47	off		131	47	off	
132	48	off		132	48	off	
133	49	off		133	49	off	
134	50	off		134	50	off	
135	51	off		135	51	off	
136	52	off		136	52	off	
137	53	off		137	53	off	
138	54	off		138	54	off	
139	55	off		139	55	off	
140	56	off		140	56	off	
141	57	off		141	57	off	
142	58	off		142	58	off	
143	59	off		143	59	off	
144	60	off		144	60	off	
145	61	off		145	61	off	
146	62	off		146	62	off	
147	63	off		147	63	off	
148	64	off		148	64	off	
149	65	off		149	65	off	
150	66	off		150	66	off	
151	67	off		151	67	off	
152	68	off		152	68	off	
153	69	off		153	69	off	
154	70	off		154	70	off	
155	71	off		155	71	off	
156	72	off		156	72	off	
157	73	off		157	73	off	
158	74	off		158	74	off	
159	75	off		159	75	off	
160	76	off		160	76	off	
161	77	off		161	77	off	
162	78	off		162	78	off	
163	79	off		163	79	off	
164	80	off		164	80	off	
165	81	off		165	81	off	
166	82	off		166	82	off	
167	83	off		167	83	off	
168	84	off		168	84	off	
169	85	off		1			

[illegible]

FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLDSKTTLTSDSVKDHTTAGRVVAGQIFLD
SEESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG
EPCHFPPFLFLDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMQEAMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMF EK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

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FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCCTGG
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAATGCCT
GTGTCCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGG
TTAATAATATTCAACATGTCAACAAC

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FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFS

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFS

FIGURE 69

GCCGCCCCGCCCCGAGACCGGGCCCCGGGGGCGCGGGGCGGGCGGGATGCGGCGCCCCGGGGCGG
 CGATGACCGCGGAGCGCACGCCGCGGGCCCCGGCCCTGACCCCGCCGCCCCGCGCTGAGCCC
 CCGCGCGAGGTCCGGACAGGCCGAGATGACGCCGAGCCCCCTGTTGCTGCTCCTGCTGCCGC
 CGCTGCTGCTGGGGGCTTCCCACCGGCCGCGCCGCCCCGAGGCCCCCAAAGATGGCGGAC
 AAGGTGGTCCCACGGCAGGTGGCCCCGGCTGGGCCGCACTGTGCGGCTGCAGTGCCCACTGGA
 GGGGGACCCGCGCCGCTGACCATGTGGACCAAGGATGGCCGCACCATCCACAGCGGCTGGA
 GCCGCTTCCGCGTGCTGCCGCAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGGC
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACCCTCGTCTGT
 GCTGGATGACATTAGCCCAGGGAAGGAGAGCCTGGGGCCCCGACAGCTCCTCTGGGGGTCAAG
 AGGACCCCGCCAGCCAGCAGTGGGCACGACCGCGCTTCACACAGCCCTCCAAGATGAGGCGC
 CGGGTGATCGCACGGCCCCGTGGGTAGCTCCGTGCGGCTCAAGTGCGTGGCCAGCGGGCACCC
 TCGGCCCCGACATCACGTGGATGAAGGACGACCAAGGCTTGACGCGCCAGAGGCCGCTGAGC
 CCAGGAAGAAGAAGTGACACTGAGCCTGAAGAACCTGCGGCCGGAGGACAGCGGCAATAC
 ACCTGCCGCGTGTCGAACCGCGCGGGCGCCATCAACGCCACCTACAAGGTGGATGTGATCCA
 GCGGACCCGTTCCAAGCCGCTGCTCACAGGCACGCACCCCGTGAACACGACGGTGGACTTCG
 GGGGGACACAGTCCCTTCCAGTGCAAGGTGCGCAGCGACGTGAAGCCGGTGATCCAGTGGCTG
 AAGCGCGTGGAGTACGGCGCCGAGGGCGCCACAACCTCCACCATCGATGTGGGCGGCCAGAA
 GTTTGTGGTGTGCTGCCACGGGTGACGTGTGTCGCGGCCGACGGCTCCTACCTCAATAAGC
 TGCTCATCACCCGTGCCCGCCAGGACGATGCGGGCATGTACATCTGCCTTGGCGCCAACACC
 ATGGGCTACAGCTTCCGCAGCGCCTTCCTCACCGTGCTGCCAGACCCAAAACCGCCAGGGCC
 ACCTGTGGCCTCCTCGTCCCTCGGCCACTAGCCTGCCGTGGCCCGTGGTTCATCGGCATCCCAG
 CCGGCGCTGTCTTCATCTGGGCACCCCTGCTCCTGTGGCTTTGCCAGGCCCAGAAGAAGCCG
 TGCACCCCGCGCCTGCCCTCCCCCTGCCCTGGGACCCGCCCGCCGCGGACGGCCCCGCGACCG
 CAGCGGAGACAAGGACCTTCCCTCGTTGGCCGCCCTCAGCGCTGGCCCTGGTGTGGGGCTGT
 GTGAGGAGCATGGGTCTCCGGCAGCCCCCAGCACTTACTGGGCCAGGCCAGTTGCTGGC
 CCTAAGTTGTACCCCAAACCTCTACACAGACATCCACACACACACACACACACTCTCACAC
 AACTCACACGTGGAGGGCAAGGTCCACCAGCACATCCACTATCAGTGCTAGACGGCACCGT
 ATCTGCAGTGGGCACGGGGGGGCGGCCAGACAGGCAGACTGGGAGGATGGAGGACGGAGCT
 GCAGACGAAGGCAGGGGACCCATGGCGAGGAGGAATGGCCAGCACCCAGGCAGTCTGTGTG
 TGAGGCATAGCCCCTGGACACACACACACAGACACACACACTACCTGGATGCATGTATGCAC
 ACACATGCGCGCACACGTGCTCCCTGAAGGCACACGTACGCACACGCACATGCACAGATATG
 CCGCCTGGGCACACAGATAAGCTGCCCCAAATGCACGCACACACAGACACAGACATGCCAGAAC
 TACAAGGACATGCTGCCTGAACATACACACGCACACCCATGCGCAGATGTGCTGCCTGGACA
 CACACACACACGGATATGCTGTCTGGACGCACACACGTGCAGATATGGTATCCGGACACA
 CACGTGCACAGATATGCTGCCTGGACACACAGATAATGCTGCCTTGACACACACATGCACGG
 ATATTGCCTGGACACACACACACACACACGCGTGCACAGATATGCTGTCTGGACACGCACAC
 ACATGCAGATATGCTGCCTGGACACACACTTCCAGACACACGTGCACAGGCAGATATGCT
 GCCTGGACACACGCAGATATGCTGTCTAGTCACACACACACACAGCAGACATGCTGTCCGGACAC
 ACACACGCATGCACAGATATGCTGTCCGGACACACACACGCACGCAGATATGCTGCCTGGAC
 ACACACACAGATAATGCTGCCTCAACACTCACACACGTGCAGATATGCTGCCTGGACACACACA
 TGTGCACAGATATGCTGTCTGGACATGCACACACGTGCAGATATGCTGTCCGGATACACACG
 CACGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGACACACATGCACACACAGGT
 GCAGATATGCTGCCTGGACACACACACAGATAATGCTGCCTCAACACTCACACACGTGCAGA
 TATTGCCTGGACACACACATGTGCACAGATATGCTGTCTGGACATGCACACACGTGCAGATA
 TGCTGTCCGGATACACACGCACGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGA
 CACACATGCACACACAGGTGCAGATATGCTGCCTGGACACACGCAGACTGACGTGCTTTTGG
 GAGGGTGTGCCGTGAAGCCTGCAGTACGTGTGCCGTGAGGCTCATAGTTGATGAGGGACTTT
 CCCTGCTCCACCGTCACTCCCCCAACTCTGCCCGCTCTGTCCCCGCTCAGTCCCCGCTC
 CATCCCCGCTCTGTCCCCTGGCCTTGGCGGCTATTTTTGCCACCTGCCTTGGGTGCCCAGG
 AGTCCCCTACTGCTGTGGGCTGGGGTGGGGGACAGCAGCCCCAAGCCTGAGAGGCTGGAG
 CCCATGGCTAGTGGCTCATCCCCAGTGCATTCTCCCCCTGACACAGAGAAGGGGCTTGGTA
 TTTATATTTAAGAAATGAAGATAATATTAATGATGGAAGGAAGACTGGGTGCAGGGAC
 TGTGCTCTCTCCTGGGGCCCCGGGACCCGCTGGTCTTTTACGCCATGCTGATGACCACACCCC
 GTCCAGGCCAGACACCACCCCCACCCCACTGTGCTGGTGGCCCCAGATCTCTGTAATTTTA
 TGTAGAGTTTGAAGCTGAAGCCCCGTATATTTAATTTATTTTGTAAACACAAAA

FIGURE 70

MTPSPLLLLLLPPLLLGAFPPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK
ESLGPDSSSSGGQEDPASQQWARPRFTQPSKMRRRVIA RPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA
TSLPWPVVGIPAGAVFILGTL LLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTHSHTHSHVEGKV
HQHIHYQC

CCACGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAAACTTCCACAGGGGACCGCATTCACAGAGTCA
AGTGACTCTGTGAAGCACCCACATCTACCTCTTGCCACGTTCCACAGGGCTTGGGGGAAAGATGGTGGGGACCA
AGGCCCTGGGTGTTCTCCTTCTGGTCTCGTGAAGTACATCTGTGTTGGGGAGACAGACGATGCTCACCCAGTCA
GTAAGAAGAGTCCAGCGCTGGGAAGAAGAACCCAGCATCTTTGCCAAGCGCTGCCGACACCTGGAGAGCCCTGG
TGAGTGGACAACATGGTTCAACATCGACTACCCAGGCGGGAAGGGCGACTATGAGCGGCTGGACGCCATTGCGT
TCTACTATGGGACCGGTGTATGTGCCGTCCCCGTCGGGTAGAGGCTCGGACCACTGACTGGACACCTGCGGC
AGCACTGGCCAGGTGGTCCATGGTAGTCCCCGTGAGGGTTCTTGGTGCCTCAACAGGGAGCAGCGGCTGGCCA
GAACCTGCTCTAATTACACCGTACGCTTCTCTGCCACCAGGATCCCTGCGCCGAGACACAGAGCGCATCTGGA
GCCCATGGTCTCCTCGGAGCAAGTGCTCAGTGCCTGTGGTGCAGACTGGGTCCAGACTCGCACACGCACTTTCG
TTGGCAGAGATGGTGTGCTGTGAGTGCAGGCGAGGCAAGAGGGTCAGCACTGCATGGCGCAGGACTGTACAGC
CTGTGACCTGACCTGCCAATGGGCCAGGTGAATGCTGACTGTGATGCCTGCATGTGCCAGGACTTCATGCTTC
ATGGGGCTGTCTCCTTCCCGGAGGTGCCACGCTCAGGGGCTGCTATCTACCTCTGACCAAGACGCCGAAC
CTGCTGACCCAGACAGACAGTGTATGGAGATTCCGAATCCCTGGCTTGTGCCTGATGGCAAAAGCATCCTGAA
GATCACAAGGTCAAGTTTGCCCCATTGTACTCACAATGCCAAGACTAGCCTGAAGGCAGCCACCATTCAAGC
CAGAGTTTGTGTGGGCGAGAGACTCCATACATGGTGATGAACCTTGAGACAAAGACGAGAGCTGGGCAGAGC
GTGTCTCTGTGCTGTAAGGCCACAGGGAAGCCAGGCCAGACAAGTATTTGGTATCATAATGACACATTGCT
GGATCCTTCCCTCTACAAGCATGAGAGCAAGCTGGTGTCTGAGGAACTGCAGCAGCACCGAGCTGGGGAGTACT
TTTGGCAAGGCCAGAGTGATGCTGGGCTGTGAAGTCCAAGGTTGCCAGTCTGATTGTGATGATGATGATGATGAT
ACTCCTTGCAACCCAGTTCTCTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTTCAAGATGCCACCACTC
CTTCTACTATGACGTGGGACGCTGCCCTGTTAAGACTTTGTGACGGGCAGCAGGATAATGGGATCAGGTGCCGTG
ATGCTGTGCAAGACTGCTGTGGCATCTCCAAGACAGAGGAAGGGAGATCCAGTGCAGTGGCTACACGCTACCC
ACCAAGGTGGCCAAGGAGTGCAGCTGCCAGCGGTGACGGAACCTCGGAGCATCGTGCAGGGGCGGTGTGAGTGC
TGCTGACAATGGGAGGCCCATGCGCTTTGGCCATGTGTACATGGGGAACAGCCGTGAAGCATGACTGGCTACA
AGGGCACTTTTACCCTCCATGTCCCCCAGGACACTGAGAGCTGGTGCTCACATTTGTGGACAGGCTGAGAAG
TTTGTCAACACCACCAAGAGTGCTACCTTTCAACAAGAAAGGGAGTGCCGTGTTCCATGAAATCAAGATGCTTCG
TCGGAAGAGGCCCATCACTTTGGAAGCCATGGAGACCAACATCACTCCCTGGGGAGATGGTGTGTGAAGACC
CCATGGTGAACCTGGAGATTCCATCCAGGAGTTTCTACAGGCAGAATGGGGAGCCCTAGATAGGAAAGGTGAAG
GCCAGTGTGACCTTCTGGATCCCCGGAATATTTCCACAGCCACAGCTGCCCAGACTGACCTGAACCTTCATCAA
TGACGAAGGAGACACTTTCCCTTTCGACGTATGGCATGTTCTGTGTGACTTCAGAGATGAGGTACCTCTACA
AGCCACTTAATGCTGGCAAAGTGAAGGTCCACCTTGACTGCACAGTGGGGAGCCCTAGATGCCAGACATATCCACA
GTGAAACTCTGGTCACTCAATCCAGACACAGGGCTGTGGGAGGAGGAAGGTGATTTCAAATTTGAAATCAAAG
GAGGAACAAAAGAGAAGACAGAACCTTCTGGTGGGCAACCTGGAGATCTGTGAGAGGAGGCTCTTTAAGCTGG
ATGTTCTCTGAAAGCAGGCGGTGCTTTGTTAAGTGAAGGCTACCGGAGTGAAGGTTCTTGCTATGTGAGCAG
ATCCAGGGGGTGTGATCTCCGTGATTAACCTGGAGCCTGAACTGGCTTCTTGTCCAACCTAGGGCCTGGGG
CCGCTTTGACAGTGTATCACAGGCCCCAACGGGGCTGTGTGCCCTGCTGTGATGACGAGTCCCCCTGATG
CCTACTCTGCCTATGTCTTGGCAAGCTGGTGGGGAGGAAGTCAAGCAGTGGAGTCTTCTCCTAAATTC AAC
CCAAATGCAATTTGGCGTCCCTCAGCCCTATCTCAACAAGCTCAACTACCGTCCGACGGACCATTGAGGATCCACG
GGTTAAAAAGACAGCTTTCCAGATTAGCATGGCCAGGCCAAGGCCCACTCAGCTGAGGAGAGCAATGGGCCCCA
TCTATGCTCTTGTAGAACCTCGGGCATGTGAAGAGGCCACCACCGATGCAGCCCACTTCGGTTCTACAGATT
GAGGGGGATCGATATGACTACAACACAGTCCCCCTCAACGAAGATGACCTATGAGCTGGACTGAAGACTATCT
GGCATGGTGGCCAAAGCCGATGGAATTCAGGGCTGTCTATCAAGTGAAGATTGTGGGGCCACTGGAAGTGA
ATGTGCGATCCCGCAACATGGGGGCACTCATCGCGCAGCAGTGGGAAGCTGTATGGAATCCGAGATGTGAGG
AGCACTCGGGACAGGGACCAGCCCAATGTCTCAGCTGCTGTGAGTCTCAAGTGCAGTGGGATGCTCTATGA
TCAGGACCGTGTGGACCGCACCTGGTGAAGGCTCATCCCCAGGGCAGTGGCTCGAGCCAGTGTGACACCCCA
TGCTGCATGAGTACCTGGTCAACCACTTGCCACTTGCACTCAACAACGACACACAGTGAATACCATGCTGGCA
CCCTTGACCCACTGGGCCACAACATATGGCATCTACACTGTCACTGACCAGGACCTCGCACGCCCAAGGAGAT
CGCGCTCGGCGGGTGTCTTGATGGCACAATCCGATGGCTCCTCCAGAATCATGAAGAGCAATGTGGGAGTAGGCC
TCACTTTCAACTGTGTAGAGAGGCAAGTAGGCCCGCAGAGTGCCTTCCAGTACCTCAAAGCACCCAGCCAG
TCCCCTGCTGCAGGCACTGTCCAAGGAAGAGTGCCCTCGAGGAGGCAGCAGCGAGCGAGCGAGGGGTGGCCAGG
CCAGGTTGGAGTGGTGGCCTCTCTGAGATTTCCTAGAGTTGCTCAACAGCCCTGATCAACTAAGGTTTTGTTG
ACTTCACTCTCTTCTGCGCTCATTTCTCATGTGACAGCCATTGTGAGACTGATGCACAACTGTCACTTGGTTAAT
TTAAGCACTTCTGTTTTCTGTGAATTTGCTTGTGTTTCTTTCATGCTTTACTTCTCTTGTCCCTGCTACTGA
TTTGGCAGTGGCCCCCACAATGGCACAATAAAGCCCTTTGTGAACTGTTCTTTAAATGAACACAAGAAATTT
GGCCACTGGTAAAACTCTGACGTTCAACTGTACTTCATTTAATGCCATTAATGCAATATACTTCTCTTCTT
TTTGCATGGTTTTTGGCCACCTCTGCAATAGTGATAATCTGATGCTGAAGATCAAATAACCAATAAAGCATAT
TTCTTGGCTTGTCTCACAGGACATAGGCAAGCCCTTGATCATAGTTTCATACATATAAATGGTGGTGAATAAAG
AAATAAAACAATACTTTTACTTGAAATGTAAATAACTTATTTATTTCTTTGCTAAATTTGGAATTTCTAGTGC
ACATTCAAAGTTAAGCTATTAATATAGGGTGATCATAGTTCTCTTACCAAGCTGGAAAGAACATCTCCTGGT
ATCCCAATTAACACAGGTGTGCTAAGTGTATTTGTACATTTCCCTTTGCAATTCGCTTTTGTCTTGTAGAAC
CCAGTGTAGCCAGGGCAGATGTCAATAAATGCATACTCTGTATTTGCAAAAAA

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI
DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQ
RPGQNC SNYTVRFLCPPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAIYLLTK
TPKLLTQTDSDGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQQHQAG
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQ NATNSFY YDVGRCPV
KTCAGQQDNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKECSCQRCTETR SIVRGRV
SAADNGEPMRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVLPFN
KKGSAVFHEIKMLRRKEPIT LEAMETNII PLGEVVGEDPMAELEIPSR SFYRQNGEPYIGKV
KASVTFLDPRNISTATAAQTD LNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
DVPESRRRCFVKVRAYRSE RFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
CVPAFCDDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPR
VKKTAFQISMAKPRPN SAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPVFN
EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVR SRNMGGTHRRTVGKLYGIRDVRS
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGSCRRASVNPMLHEYLVNHLPLAV
NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFPRVA
QQPLIN

FIGURE 73

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC
 AATATCTTAACTCTTCATATTTGGTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCTACCTACCCGTACGCATACATACATATGTGTATATATATGTAACTAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAGAAGATTACAAAGAATTTAGAGATGATTTGTCAAGATCCCTGTCGATTCATG
 CCCTTTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCTTTGGTTTGGGGACATTATGATTTGTGTAAGACT
 CAGATTTACACGGAAGAAGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAATA
 TCTGAAAGTGAAACTCGATCCTCCGGATATTACCTGTGGAGACCCTCCTGAGACGTTCTGTGCAATGGGCAATC
 CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTGAATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGAAGGAGTATCCCAAGCCTCTCCAGGTTAACAT
 CACTCTGTCTTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTTCACATGGATCCTAAATCCGTGAAGGATTTATCACAGCATAACGGTCTTAGAAATCATTTGCACAGA
 AGAGTACTCAACAGGGTATACAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTTCGCGCTTTTGG
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT
 ACAGTCACAGACCTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAAATATTTGTAGATGAGCTACACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAATCTCCATGCCACTGTATGTG
 TGTATGACAACAGCAAATTGACATGCGAATGTGAGCACAACACTACAGGTCCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAAGGCACGTGCAATACCTGTATCCC
 CAGTATTTCCAGTATTGGTACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGGACGTGCCACA
 ACAACGTGCGCTGCTGTGCCCGGCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCCGCACGGCACCCCGAGCGTGCTGCTGCTGACCACGCTGCT
 GGGAACCGCCAGCCCCCTGGTGTCTTAGGTGTACCTCCAGCCACACCGGACGGGCCTGTGCCGTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAACATAGGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCCTAACTGAACATAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTT
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAATCACATTGCCAGCTGCAGAGCATATTGTGGA
 TTGGAAAGGCTGCGACAGCCCCCAACAGGAAAGACAAAAACAAACAAATCAACCGACCTAAAAACATTTGGC
 TACTCTAGCGTGGTGCGCCCTAGTACGACTCCGCCCAGTGTGTGGACCAACCAATAGCATTTCTTTGCTGTGAG
 GTGCATTGTGGGCATAAGGAAATCTGTTACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAACCCTCGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGCACA
 TGTGTAACAGCCCCCTCTAAAAGCGCAAGCCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA
 GCACACACCCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCTTTTGTATTCAAATGAAGTT
 ATTTTCTTGAACACTGTAATATGTAGATTTTTTGTATTATTGCCAATTTGTGTTACCAGACAATCTGTTAAT
 GTATCTAATTCGAATCAGCAAAGACTGACATTTTATTTTGTCTCTTTTCTGTTTGTCTTCACTGTGCAGA
 GATTTCTCTGTAAGGGCAACGAACGTGCTGGCATCAAAGAATATCAGTTTACATATATAACAAGTGTAATAAGA
 TTCCACCAAAGGACATTCTAAATGTTTTCTTGTGCTTTAACACTGGAAGATTTAAAGAATAAAAACTCCTGCA
 TAAACGATTTTCAGGAATTTGTATTGCAATTTCTTAAGATGAAAGGAACAGCCACCAAGCAGTTTCACTCACT
 TTAAGTATTTCTGTGTGGACTGAGTACATTGAGCTGACGAATTTAGTTCCAGGAAGATGGATTGATGTTCACT
 AGCTTGGACAACCTTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACAACAGCAAAAAAAAAAAAAA
 AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGTANTCIPSISISIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
PLVF

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCGGCTAAGATTGCTGAGGAGGCGG
CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCGTCCGGGCGAGGTGTCCTCATGACTT
CTCTTGTGGACC**ATG**TCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC
CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGGAAATGGAGGAGACGGCTCA
AGAGTTTAGCCTTGCGACTGGCCCAGTATCCAGGTGAGGTTCTGCAGAAGGTTGTGACTTT
AGTATACATTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
AGCAGCCATGGCCTTCTGCTTCTGAGACCCTGTGGTGGGAATTCACAGCTTCCTATGACA
CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAG
AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
ATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA
CCAGTGACAGCCCTGGGTATCCTCTCCCTCATCTCAACATCATGTGTGCTGCCCTGAATCT
CATTCGAGGAGTTCACCTTGCGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
TGGACCAAACCTCG**TGAG**CCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
AAAGGGCATGTCAGTGAAATCTGGGAATGGCTGGATTCCGAAACATCTGCCCATGTGTATTG
ATGGCAGAGCTGTTGCCCAAGCGCCTTTTATTTAGGGTAAAATTAACAAATCCATTCTAT
TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTT
GCTTCAGAAGTGTTATTTTCATGAATCATTCATATGATTTGATCCCCCAGGATTCTATTTTGT
TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTT
TTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAACTCAGTAGTACAACC
TAACTTGTATAAAAGTGTAATAAATGTATAGCCATTTATATCCTATGTATAAATTAATG
AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTATTATAAAAAAAAAAAAAAAAAAAAA
AAAAG

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FIGURE 76

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIIRGVHLAEHSLQDPRSWFCWLDQTS

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FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

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FIGURE 78

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG
 CCTGCCCCCTTAAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTT
 TCTGTGCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGCGGCTT
 CCTCCCCGCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGAACACTGTACATCCTCTGCCACATCTTCCTGAC
 CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCTCGGAACTACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA
 TCTTCCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
 GGTGTCCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCCCTACCTCTACTCATGCATCTCCTTCCTTGGGGTTCTG
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGAGGATCTGTAATCCTACTTCCTGCTGGCTGCCTTTAGACATGGAGCTG
 CTACACAGACAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGC
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGGTGGTGGTGGTGG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTCAATCAGGTTGTACTCATCTTTTACCTAATGGTGTCTCAGTTGTGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCACGACACTGCCATGACGCAGATAATT
 GGGAACTGTGTCTGTCTCCTGGTCCCTAAGCTCAGCACTTCCTGTCTTCTCTCGAACCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTTCTCTACAACGCAGCCTTTGCAGGCCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCTTTGGGCTGGACAGACTGCCGCTGCCCGT
 CTCCGGTTTCCCCCAGGCATCTAGGAAGACCCAGCACCACT**TGAC**CCTCCAGCTGGGGGTGGGA
 AGGAAAAAACTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATT
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAAGTGTGGCCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCCCTGATCCCAAATCTGTTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGATGTGCAAT
 AGGGTGGGGTAGGGGAGGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 CTTGCCTCTGGCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACCTG
 AAAGACCAAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCCAGGGA
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FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTSESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYPYLYSCISFLGVLLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSFGAVIQVVLI FYLMVSSVVG FY
SSPLFRSLRPRWHD TAMTQIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLG NFY
IVFLYNAAFAGLTTLCLVKTF TA AVRAELIRAFGLDRLPLPVSGFPQASRKTQH Q

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FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTC**ATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCCATT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCCAGACAATATCCTTGAGGTTGAGGAATCTGGAGAGTACAGATGCCAG
CCCCAGGGCTCCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCT**TAG**GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
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FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLOPPWTTVFQGERVTLTCKGFRFYSPQTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLD FSSEM GFPHAAQANVELLGSSDLLT

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FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGT
GAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAG
GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCA**ATG**GCTCCGCAGAACCTGAGCACCTTTT
GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
GGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA
GCTTCATCCCGACCGGAACCCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG
CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA
GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTT
TGGTTTTCATGTTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA
TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGCAAGAGAT
GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
AGATTTACGGTTCCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT
TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT
ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
TCACTTTTGTATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATAT**TGA**GAGTG
AATAAAATTGGACTTTGTTTAAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTTCGGAAAAGAATGACC
AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCTGAGT
TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
GTTGTTAGCAATTTCAATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
TTATTTT

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQ
AQEKFDLGAAYEVLSDSEKQYDITYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ
DRNIPRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVCDCEPNVKLVNEERTLEVEIEPGVRDGM EYPFIGEGEPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGSIIITFDVDFPKEQLTEEAAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTAAAAAGG
CCTATAGGAACTAGCCCTGCAGNTTATCCCGACCGGAACCCTGATGATCCACAAGCCCAG
GAGAAATTCCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTAAAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

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FIGURE 87

GGCACGAGGCGGCGGGGAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
CTCTGCAGGTGTCTGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC
TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
AGAGAAGCTTGTTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
TACCCTCCGTTGGACCCCCAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTCTGAG
TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC
AGTCTCTGTCTGGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
CCAGATAAAGGCCTCCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTT**TAGT**GCCT
ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
TAAAGCAGGAGATCCCCGTAGTTTATGCCTCTTTTGAGTTGCAAACTGTGGCTGGTGAGT
GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT
AAGAAATCAAGAGGTTTCACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTCAGAATG
TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC
TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT
GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGAGGTTTGGGTTTGAAGCTGAGGAACT
ACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

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FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCGAGGTGCTTTCGCCGCTGTCC
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTTTTCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
TGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAGAACATTTCAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTTCTGGGTGGTGTATTTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTTCAG
GGGCTTCTTTCCTGTCTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATAACAACA
AGTGAATTTGAAGACTCATTTAAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
CTGTGGTGCCTGTTTCTTTTCTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAAACCAAGGAAACCCCAATTTTG
ATGTATGGATTACTTTTTTTTTGNGCNCAGGGCC

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FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLEFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTTCCTGTTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

TCTCTTGTTT

FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
GGCTGCCAGGAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGGACTGC
TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
ATCAACACCATTTCAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA
GATCAACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTTCACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAGTTTGACGACCTCCGGGACTACCCCGAGAAGTATTTTTTTCCT
GATTCAGTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
GGGCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTTCAGAAA
TAATGAAAATCCAACACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA
GACGCCCATGGTGCCCCCCCCGGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCTCGC
TGGTGCTCTACCCTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT**T**
GACTCAGGGAGGTGTCACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCTGCTGGGCACGGCGGAAGTCACGA
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT
TTTTCCCCATGTGCTTTAGTGGGCTTTGGTTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGTGAACCTTTGTTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCCTTTTCATCCTTTGGTGCTGAGTTTTCTGT
AACCCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC
CAAGAAAAAAAATTAAAGTGCTTTTCTGGGTCAAAAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIA SGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHNKFEIDFLCGWSLSERFGLLGSKVLAKK
ELAYVPIIGWMWYFTEMVFC SRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVNLGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS
KQKLND

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FIGURE 94

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTGGCGGTGCTCTCGGGCTTTGTGCTCG
GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA
GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA
TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG
GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
TGGTACAAATTCCGTCGTCATTTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
AACTTGCAGGAGCATTTTTTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAA
TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTTATAAAAC
TGTATCAGGTTCCGTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
CAAGAGGAATTAAAGAGTATATGCAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACT
AGTAAAGGATGTAAACAGATTAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGG
CAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGAACATTTTTCTTTGTTCAGGCATTA
CGGACCTTTTTTCCAAATCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA
TGTTTCTAAAAGTAGCTGTAAC TACAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA
TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAGCAT
AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTTGGTGAATATTCACGGTCTCCTACA
TTT**TGA**TCCTTTTAAACCTTACAAGGAGATTTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT
TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTCAC
CTGTTTGCAGTAATACACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTTCAAAC
ATCAGATGCTTTTATTTCCAAACCTTTTTTTTACCTTTCACTAAGTTGTTGAGGGGAAGGCT
TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
TGGGCAACGTATTGAGACCATGTCTATTAAAAAATAAATGGAAAAGCAAGAATAGCCTTAT
TTTCAAAATATGAAAGAAATTTATATGAAAATTTATCTGAGTCATTAAAATTCTCCTTAAG
TGATACTTTTTTGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
ATAAATTTGCAAAACATCATCTAAAATTTAAAAA AAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLEVKGEAKNSITDSQMDDVEVVYTIIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDDVDNLTLMEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDQTQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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FIGURE 96

GGCACAGCCGCGCGGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGC
 CCAAGCAGCGCGCAGCGAACGCCCGCCGCCGCCACACCCCTCTGCGGTCCCCGCGGCGCCTGCCACCCCTCCCT
 CCTTCCCCGCGTCCCCGCTCGCCGCGCCAGTCAGCTTGCCGGGTTCGCTGCCCGCGGAAACCCCGAGGTACCA
 GCGCGCGCCTCTGCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCTGGCCCGCGCCTGGCACC
 GGGGACCCTTGCCGTGACGCGAGGCCAGCTCTACTTTTCGCCCGCGTCTCCTCCGCTGCTCGCCTCTCCAC
 CAACTCCAACCTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCCCGTGCCGTAG
 CGCCGCTTCCCGTCCGGTCCCAAAGGTGGGAACGCGTCCGCCCGGCCCGCACC**ATG**GCACGGTTTCGGCTTGCC
 CGCGCTTCTCTGCACCCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG
 AAGTGCGACGCTTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTACGTTACAAGAAGTTTG
 ATGAATTCCTTCAAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAATTTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
 CGCAAATTAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTACTTTGCTCAAGGCTTAGCGGTTGCGGG
 AGATGTGCTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTAACCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCCGGGGTCTCGTGACTGTGAAGCCATGTTACAACACTACTGCTCAAACATCATGAGAGGCTGTTT
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCTTTCAACATTGAATCGGTGATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG
 ATAATAGTGTTCAAGTGCTCAGAAGGTTTTCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATT
 TCTCGTTCATCTCTGAAAGTGCCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACCACAGC
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGGTCCT
 CCCTTCCGAGCAACGTTTGAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGG
 AAAGGCAAAGCAGGTACCTGTTTGCAGTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCAGAGGTCCA
 GGTTGACACCAGCAAACCAGACATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA
 AGAATGCATACAATGGGAACGACGTGGACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAAGT
 GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGAATACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGA
 GAAAGCCGACAGTGCTGGTGTCCGTCTGGGGCACAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGG
 TTATGCAGAGAGAGTGGAGAT**TAA**TTCTCAAACCTCTGAGAAAAAGTGTTTCATCAAAAAGTTAAAAGGCACCAGTT
 ATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAATGGACAACAATGTACAGTTTCTACTATGTGGC
 CACTGGTTTAAAGAGTGCTGACTTTGTTTTCTCATTCAAGTTTGGGAGGAAAAGGGACTGTGCATTGAGTTGGT
 TCCTGCTCCCCCAAACCATGTTAAACGTGGCTAACAGTGAGGTACAGAACTATAGTTAGTTGTGCATTTGTGA
 TTTTATCACTCTATTATTTGTTTGTATGTTTTTCTCATTTTCTGTTTGGGTTTTTTTTTCCAACGTGTGATCT
 CGCCTTGTTTCTTACAAGCAAACCAGGGTCCCTTCTTGGCACGTAACATGTACGTATTTCTGAAATATTAAATA
 GCTGTACAGAAGCAGGTTTTATTTATCATGTTATCTTATTAAGAAAAAGCCCAAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSINDMF
VKTYGHLYMQNSSELFKDLFVELKRYVVGNNLEEMLNDFWARLLERMFRVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQGC GPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCG**ATG**AAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTTCATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTG**TAG**GAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCCACCTCACTCTCCCACTGTACCCACC
CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTGTTGCTCTC
TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCAGGAACTGTAGCTTCCTAGCTAGTGTCAATTAACCTTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

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FIGURE 99

MKVLISL L L L L L P L M L M S M V S S S L N P G V A R G H R D R G Q A S R R W L Q E G G Q E C E C K D W F L R A P R R
K F M T V S G L P K K Q C P C D H F K G N V K K T R H Q R H H R K P N K H S R A C Q Q F L K Q C Q L R S F A L P L

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FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTTTGCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

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FIGURE 101

MAVLVLRRLTVVLGLLVLFLTCYADDKPKDPDDKPDGSGKDPKPDFPKFLSLLGTEIIEHAVE
FILRSMRSTGFMEFDDNEGKHSSK

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FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTAC
CCTGCCCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAGCTACTTCC
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
CTGCGGAACCGGAGCCAACTTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACTCTGGTGCTGTGCTCTGTGCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCC
GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCCTTCATGTGGCAGCAAGTTTTTCGAGCCCACCTGGAAACACATTGGGGATGGCTG
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
CTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCT
CTCCCCACTACCACCTTCTTCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
AACCACG

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FIGURE 103

MDILVPLLQLLVLLLTPLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELF SQI
KGLTGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLEFFWEHVAEPYGSWAFM
WQQVFEPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPVGPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIYLPLRGT

FIGURE 104

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGGAAGTTGCCTCATCGCAGG
CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAA
TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATCTG
AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACTCGCTCCAAT
GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAAACTTTTGGAAGGAA
AAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
TTGCCAATTCTGGTTCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
AAGATTGTGATTTCAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTAC
ATTGGCTATCTTGACTATAAAAAGGAAAGAATTCGTAAGCTTTCCATGAAAGCCAGCACTTG
CTCATTTAATCCTGGAGTTTTTTGTTGCAAACCTGACGGAATGGAAACGACAGAATATAACTA
ACCAACTGGAAAAATGGATGAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
GGTAGCATCACAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
TATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTA
AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTCAACCTAATCCGAAG
ATATACCGAGATCTCAAACATAAAGTGAAACAGAATTTGAACTGTAAGCAAGCATTTCTCAG
GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
GCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT
ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA
TAATTCAAACCTGCTGTTGGTTTTAATTTTGTAACCTGTGGCCTGATCTGTAAATAAACTT
ACATTTTTC

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTD SGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINS IQHNTRS NVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKV VIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNITNQLEKWMKLNVEEGLYSRTL AGSITTPPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKA AKLLHWNHGLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTCAGCACAACACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCACAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
GAGCTAGAGGGCAAGTGTGCTCGGCCCAGCGTGCAAGGAACGCGGGCGGCCAGACAACGGGC
TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGGCGCGGGCTGCA
TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
TGTCGGAGCCCTAACCAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT
TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
CCGTAAAGTAAACATCATCATCTTGGTCCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
CATAACTTCCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTCAGGAATTGTAG
GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
ACAGCATTCAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
GCAGACCATCTCCGGTCTTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
TCAATTTTGACCCTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCAGCGCAAAGAAGG
CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
CTGAAGCCAGGACATGCAGCTGCATTTTCAAGATTGTGATTCAGCCTCTACTAAAGTTGT
CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
CTGACGGAATGGAAACGACAGAATATACTAACCAACTGGAAAAATGGATGAACTCAATGT
AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
GCTGGAAAACGATATTCACCTCAGTTTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACA
TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA
GACCCAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
CAGAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCCTGGAAGATAGCATGCGTGGGAAG
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAG
GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAAT
ATGTCTCCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA
CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTTT
GTAACCTGTGGCCTGATCTGTAAATAAACTTACATTTTTCAATAGGTAAAAA
AAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTGCCTGTCATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCCTGTCCTGAGAAGGCCCCACCACCCAGAACCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCCCTGGCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCCCTCCCCTGGTCCTCCCAGTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

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FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
GTTCCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
CTCCCTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAA
TC**ATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGCTTTGGCC
ATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTCAATTGGTTAT
TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATAACCAACGACC
TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTA
TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT
GACAGTTGAGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC
AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
AGCCTGGGAAGTGCAGGAGCTGCCCAGGTTATGGAAGGCGGCCAAGTGGAATATAAGCCCCT
TTCGGGCATTTCGGTACATGTGGTTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT
AAAAATGATCCTCCTGATCATCCCATCCTTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA
AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCCGAGAATCATTGTCA
TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
TGTCCAAGAACTCAAGTCACTTTACATCTATTAACCTGCTTTGGAGACTTCATAATTTTTCTA
GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGCCTACTTAGTAGCCC
ATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCCTGTGTTTTGCTGTTGAT
CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
CGTAAAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGA
ATGAGGAGGGGAACAGAACTCCAGGCCATTGTGAGA**TAG**ATACCCATTTAGGTATCTGTACCT
GGAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
AGTGAATTTTTTTTTTAAAAGACCTAATAAACCTATTCTTCCTCAAAA

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FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQOMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

[illegible]

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FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNRPRADPGIQ
RQDPGGAFFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNDRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLOPLVKRVCDTDRDLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTRIGAVQYTYEQRLEFGFDKYSSKPD
LNAIKRVGYWSSGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSEFFVDEFNLHQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCCGCCCACTACAGTTTTTCTCTGACTCTAAT
TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG
TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAAACAAACATT
CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA
GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCGAAAACCTCC
TCCCAGCCTTTTACAGACCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG
AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
CACCTGAGCAGCCTCACTGGTGACCCGGTGTTTGAAGATGTGGCCAGAGTGGCTTTGATGC
GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
AAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
CCATCCGGAACCTACACCCGCTTCGATGACTGGTACCTGTGGGTTTCAGATGTACAAGGGGACT
GTGTCCATGCCAGTCTTCAGTCCTTGAGGCCTACTGGCCTGGTCTTCAGAGCCTCATTGG
AGACATTGACAATGCCATGAGGACCTTCCTCACTACTACACTGTATGGAAGCAGTTTGGGG
GGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGGCTACCCA
CTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCT
CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGCGGAT
TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCCTG
GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCACTTCATCCACAACAATGG
GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGGTACA
TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC
GAAATTTTCAAAAAACACTGTTAGTTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCT
AGACTCCTCATAACCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA
AATTGCTTTTGGCTATCATAAAA

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FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOQYTVVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCCTGGAGA
AACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTCTAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG
GGGTATTCCAGTGACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCCCTGGTACTGGCCCTGTTTGCCCTTGTTGGCTTCATGCTGATCCTTGT
GGTCGTGCCACTGTTTCGTCTGGAAAATGGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG
TGGTCCCTCCCAGACACCTTGAAAATAACCAATTCACCCAGAAAGTTAATCAGCTGCAGAAGG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT
CTCA**TAG**GTTTGCGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
TGA CTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGA CTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTCAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGAGAGGCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACCTCAAGCCCAATGCCGGTGACAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTTGTGCTCCTTTTTTC
TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
AAAAAAAAA

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FIGURE 117

MQTFTMVLEEIWTSLEFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHELLMWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS AW
SILKHPFNRNSTILTRPGMEITKDG FHLVIELEDLGPQFEFLVAYWRREP GAEHV KMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLV LALFAFVGFM LILV
VVPLFVWKMGRL LQYSCCPVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTG
GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
TCAACATCCGGGGCAAACCTGGTGTCGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
AATGTGGCCAGCGAGTGCGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGCCCCCACCCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCC
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
TGGTAGGGGCTTGGGACCCAACCTGTGTGTCAGTGGAGGAGGTCAGACCCCAGATCACAGCGCTC
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTATTAACCACCGCGTCTCCTCCTCCACCA
CCTCATCCCGCCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAG
AGACCCACTGACTCTCCTTCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG
AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA
TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAAT
AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
GTTATTTCTCCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
ACAATACCTCACGATATAAAATAAAAATGAAAGTATCCTCCTCAAAAA

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FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVNVASECGFTDQ
HYRALQQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSGKEPTWNFWKYL VAPDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATGG**GCTGTCTACGTCGGGATGC
TGCGCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGCCCGGGCCGCCCTCTCT
CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCCTCAGTTCCAGAGAGGTGGATCG
CATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTCAAGGGGTGCACCAAAAAGCATCTTA
ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
TTGGTCGTCTCCATGAAGACGTCAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA
AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC
CTAACTCCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTCTGGTG
TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAA
GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCTGAAGCAGATCT
GTCCAGAAGTGGAGAATGCCAGCCAGGGGCCTTGAAGAGTCAGAGGCTCCCAGATCTGACC
ACAGTCATCTCGGTGGATGCCCTTTGCCGGGGACCTTGCTCCTGGATGAAGTGGTGGCGGC
TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACCAGCAGTTCTGTCTGCCATG
ACCCCATCAACATCCAGTTACCTCGGGGACAACAGGCAGCCCCAAGGGGGGCCACCTCTCC
CACTACAACATTGTCAACAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
ACCAGAGCAGTTGCGGATGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCTGTGGCAG
GCACAATGATGTGTCTGATGTACGGTGCCACCTCATCCTGGCCTCTCCCATCTTCAATGGC
AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGAT
GTTTCGTGGACATTCTGAACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
GTGTCAATTGCTGGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
ATGAAGGACCTGGTGGTTGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTT
CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGG
CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGC
ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCACAATGAATGAGCAGGGCTTCTGCA
AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
CTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
CGATCGGATGGGGGAAGAGATTTGTGCCTGCATTTCGGCTGAAGGACGGGGAGGAGACCACGG
TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
GTGTTTGTACAAACTACCCCTCACCATTTCAAGGAAAGATCCAGAAATTCAAACCTTCGAGA
GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCCTGTCTGGCCGGTTGGCTT
GACTCTCTCCTGTGAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCCAGTTC
TGAGCCAGGCACATCAAATGTCAAGGAATTGACTGAACGAACTAAGAGCTCCTGGATGGGTC
CGGGAACCTCGCCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG
TCCATCCCCACATTCCCCTGTCTGTCTTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTT
GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFLLSSREVDRMVSTPIGGLSYVQ
GCTKKHLNSKTVGQCLETTAQRPVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLDEVVAAGSTRQHLDQLQYN
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTFAHFPEDTVEQKAESVG
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
MNEQGFCIVGRSKDMIIRGGENIYPAELEDFHTHPKVQEVQVVGKDDRMGEEICACIRL
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCCAACCCCTGTACCATTGCCTGGGTTCCTGTCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC
AGGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
AGTGCGGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGC
TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTG
CTACAGCTGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCTGTAGCT
GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCA
GCTAATGTGACTGTGTCTTGCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
TGGAGTAACAGGCCCAGGGTTACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACT
CTGACCTCCGCAACAAGACCTACTTCTCCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCT
CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCACCACTTCTACCTCGGCCCCAGTGAG
ACCCACATCCACCACCAAACCCATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAG
AACACGAGGCCTCCCGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC
CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGT
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
CATCACTTCCCTGTTCCCACTACTGGACTGGGCTGGCCCAGCCCCCTGTTTTTCCAACATTCCC
CAGTATCCCCAGCTTCTGCTGCGCTGGTTTTCGGCTTTGGGAAATAAAATACCGTTGTATAT
ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTG
AGAGAGAGGATGCTAAGCTTCCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGG
GAATCGGTTCCCCATATGTCTTCCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCCGGTAC
CCAATTCGCCCTATAGTGAGTCGTA

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FIGURE 125

MDPARKAGAQAAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPVVSVCYNASDHVYKGCDFGNVTLTAAANTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTTSVTTSTTSAPVRPTSTTKPMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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FIGURE 126

CGGGACTCGGCGGGTCCTCCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCC**ATG**GAGT
TGGTGCTGGTCTTCCTCTGCAGCCTGCTGGCCCCCATGGTCCTGGCCAGTGCAGCTGAAAAG
GAGAAGGAAATGGACCCTTTTCATTATGATTACCAGACCCTGAGGATTGGGGGACTGGTGTT
CGCTGTGGTCCTCTTCTCGGTTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTT
TCAATCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCCAGGTGGAGAACCTCATCACCGCC
AATGCAACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAA
CCTGAGGCGGCTGCTTGAACCTTTGGATGCAAATGTCGATGCT**TAA**GAAAACCGGCCACTTC
AGCAACAGCCCTTTCCCCAGGAGAAGCCAAGAAGCTTGTGTGTCCCCCACCCTATCCCCTCTA
ACACCATTCCTCCACCTGATGATGCAACTAACACTTGCCTCCCCACTGCAGCCTGCGGTCCT
GCCACCTCCCGTGATGTGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTG
GTCTTTGTGGCTACTTGTTTGTGGATGGTATTGTGTTTGTAGTGAAGTGTGGACTCGCTTT
CCCAGGCAGGGGCTGAGCCACATGGCCATCTGCTCCTCCCTGCCCCCGTGGCCCTCCATCAC
CTTCTGCTCCTAGGAGGCTGCTTGTTGCCCGAGACCAGCCCCCTCCCCTGATTTAGGGATGC
GTAGGGTAAGAGCACGGGCAGTGGTCTTCAGTCGTCTTGGGACCTGGGAAGGTTTGCAGCAC
TTTGTGCATCATTCCTCATGGACTCCTTTCACTCCTTTAACAAAAACCTTGCTTCCTTATCCC
ACCTGATCCCAGTCTGAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCC
CAGCGTTGACGTCAGGCAGGCTATGCCCTTCCGTGGTTAATTTCTTCCCAGGGGCTTCCACG
AGGAGTCCCCATCTGCCCCGCCCTTCACAGAGCGCCCGGGGATTCCAGGCCAGGGCTTCT
ACTCTGCCCCCTGGGGAATGTGTCCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGG
GACCCTACCCCTTCCAACCTTCCCTGCTTCTGAGACTTCAATCTACAGCCCAGCTCATCCAG
ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCC
GTTGGGGCCAGCACACCGGGATGGATGGAGGGAGAGCAGAGGCCTTTGCTTCTCTGCCTACG
TCCCCTTAGATGGGCAGCAGAGGCAACTCCCGCATCCTTTGCTCTGCCTGTGCGGTGGTCAGA
GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAG
GTTGAAGGTCATAACGAGAGTGGGAACTCAACCCAGATCCCGCCCCCTCCTGTCCTCTGTGTT
CCCGCGGAAACCAACCAAACCGTGCGCTGTGACCCATTGCTGTTCTCTGTATCGTGATCTAT
CCTCAACAACAACAGAAAAAAGGAATAAAATATCCTTTGTTTCCT

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQORTEVQPSGGS LWNLRRLLEPLDANVDA

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FIGURE 128

AAACTTGACGCC**ATG**AAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCTCTGCCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAG**T**
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA

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FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESIKRKLPFLNWDAFPCLKGLRSATPDAQ

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCC**ATG**GGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTC
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCA**TGA**GAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTATTATC
TTCATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

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FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTTCCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTTCATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGAAAATGACTGCATGTTCCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGAGCAGCACAGTG
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACCTTGTTGATGCAGAATACACCAAAAAC
 CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAACCTGAACCTATAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTTCCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTCATTTTCTTAAGACCAATC
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTAATGTAGG
 AAACCCATATGGGGTTTATGAAAAATACTTGGGGATCATCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAACCATAAACTCTGTTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYREND CMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLENFRGVAASFREFKHLFLCGSLVFHVGDEWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMD DITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

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FIGURE 134

CACCCCTCCATTTCTCGCCATGCCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTTGGGCAGC
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCTTCAG
AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCACTGGTGATGCGGTACTGGGAGCC
CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGGCCACCTGGGTGCCGC
TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCCACCTGCGCCACCCAGTGTGTG
TGGAGCTGCTGACAGTGTGTGGGTGGTGCCTACCCTGGGCACGGACCGTCTCCTCCTTGCT
TTCCTCCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
CCGGGCCCAGCTACAAAGAAACTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCCTCTCCCACTGAATTCTAAATCCTTAAC
ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATAACCCTAAATTCTGAGTTTCAGCCA
CTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
TTCCTGTTTGTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
CTGACCACTCCCCCTGGCACTGTTACTTGCTCTGCGCCTCAGGGGTCCCCCTTCTGCACCGCT
GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
GGCCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

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FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVQGHSLSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSLRHPVCVELLTVLWVPTLGTDRLLLAFLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTCACCCCGAGTGTAAGAACCCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCAGTGAATCC
 CTCAAATGGAGCCTCCTGCTGCTGTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACCTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATATGGC
 ATTCAGGTGGGTAACTGAGTTTTTGGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTATATAA
 TGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAACCAACCATCAAGTTT
 GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAAAGTGAACATTCATATTCCAGAAGA
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTATTAACTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTG
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAATATA
 TGTAGTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTAAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
 CATTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAA

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FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLTLKTIMAFRWVTEFCPNAKYVMKTD TDVFIN
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRD
LVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

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FIGURE 138

CCTCTGTCCACTGCTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS
IWDYGNGFAATRLFQKKTCTIVHKMNKEVMPSIQSLDALVKEKKLQKGPGGPPPKGLMYSVN
PNKVDDLKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

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FIGURE 140

CATTTCTGAACTAATCGTGTCAGAATTGACTTTGAAAAGCATTGCTTTTTTACAGAAGTATA
TTAACTTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCG
CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTCTTATTGCTTACTGATTTTTT
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG
CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
CAGATTCCGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAAT
CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAAGCCAACTATGAATTAC
TGGAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAAGCAAAGGGA
TTGAATCCGGATGGAAGTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC
ATCATCACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAAGAAA
GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
GGTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTTCCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT
ATGGACTCAATCAAAAACATTAACGCAAACTGATTAGGATTTGATTTCTTGAAACCCTCTA
GGTCTCTAGAACACTGAGGACAGTTTCTTTTAAAAGAACTATGTTAATTTTTTTTGCACATT
AAAATGCCCTAGCAGTATCTAATTAATAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTT
ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT
ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTTTACAAGGAAATAAAATACAAAT
CTTGTTTTTTCTAAAAAATAAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKSRRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRGHGRHR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNNTATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTTACAGAAATATAT
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGTGGTTTGTTCATGCA
AGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAAGCCAAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAAAGCAAAGGGATT
GAATCCGGATGGAAGTCCAGCCCTTCAACCCTGGGTGGATTTTCTCC

FIGURE 143

GGCACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGTCATGGC
GGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTTTGTTCGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCAGCTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCCTGGAGTACCAGTGG
TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTCACAGAGGCCTACTACTACAT
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
GGAGGAGACCCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCCTGTGGCCAAGCTGGCTATCCGCGTG
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCCAGGCCTGCGGCTGGC
CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCCTCCTGC
ACACCAGCTTCCTGTCTCCCCTGTTTCATCCTGTGGCTCTGGACAAAGCCCATTGCACGGGAC
TTCCTGCACCAGCCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGCTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC
ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCCTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTGGGGCCTGGGCCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
GGCCCTGGGTGGCCTGCTTACTCCCCTCTTCCTCCGTGGCGTCCTGGCCTACCTCATCTGGT
GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA
GGCTCCTAGCTGCCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
CTAGCCTGCCCCCTCTGTTTGCGCCCGCTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC
GGCGTTCCCTTCACCACAGTGCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
GAACTGTCTCTCCTGGGCCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG
TGCCAGGTTTGTAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
GATTTTTAA

FIGURE 144

MAVLGVQLVVTLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGGERSVCLTFAFLFLLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGWDWALPVAKLAI RVGLAVVGSVLGAFLTFFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FD SGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVS LQYLTPLILT LNCTLLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLA GS

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FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATAACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCCCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

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FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAACGTGGCTT
 AATCTGAAGGTTCTCAGTCAAATTCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGG
 CGCTTCTGTTGCTGGTCTTGCCCTTGGCTCAGTCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTG
 TATTCAAGACTCTGTAAAGGTGCCTCCCCTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTG
 TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCCTGGCCTAGACAACCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAAGTGGGACAGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAAATAAATCGAGCTTTGAGTGTCTTTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGG
 GCAGGGAAAAATTCTGAAAAACCACTGCCCCCTGAAGTCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAA
 ATTACCAGCATCAAGATCAATCGAGTAGATCCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCCTGCGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCGCAGCAGGAACAATGGACAGGCCCC
 GGATGCCTACAGACCCCGAGATGACAGCTTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGAA
 TAAAACTGGTGGCAAGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCAGAAAG
 TGCGGCTCATCTGATTAGGCCAGTGAAAGACGTGTTACCTCGTGTCCCGCCAGGTTCCGCAGCGGAGCC
 CTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACT
 CCCAAGCCCCCTCATCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGCAGGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCATCAGTGTGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAAGTGA
 GAGGTGAGCCGGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCA
 GTGACTGGTCCCCATCCTGGGTGATGTGGCTGGAATTACCACGGTGCTTGTAACGTAAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAAACAAACCTTT
 TTTTCATCAAATCCATTGTTGAAGGAACACCAGCATACAATGATGGGAAGATTAGATGTGGTGATATTCTTCTTG
 CTGTCAATGGTAGAAGTACATCAGGAATGATACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGA
 ATTACTCTAACTATTGTTTTCTTGGCCTGGCAGTTTTTTATAGAATCAATGATGGGTGAGGAAAAACAGAAAAA
 TCACAAATAGGCTAAGAAGTTGAAACACTATATTTATCTTGTGCAGTTTTTTATATTTAAAGAAAGAAATACATTGT
 AAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAAAATATGATTCCAAAAAATTA
 AAATACTAGTTTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTACAACATTGTTTTATATTTTTTCTATTCAAT
 AAAAAGCCCTAAAACAATAAATGATTGATTTGTATACCCCACTGAATTCAAGCTGATTTAAATTTAAATTTT
 GGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTTAATTTACAGCTAAAATATTTTTTAAATGCA
 TTGCTGAGAAACGTTGCTTTCATCAAACAAGAATAAATATTTTTTCAGAAGTTAAA

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FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVD SGRSNRTRARPFERSTIRSRS
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHIIIIQHIIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQ LGIKLVRKVDEPGV
FI FNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESA AHLIQASERRVHLVVS RQVRQRS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKV VNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

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FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAA**ATG**GTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTCAAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCATGTT**TAG**GATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAAGTCAAATTAAATTCTTTCCCAATGCCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTTATA

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FIGURE 149

MKILVAFLVVLTIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSST
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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FIGURE 150

GGCACGAGCCAGGAACTAGGAGGTTCTCACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTCCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACCTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
GATGATCTGCCAGGCGTCCTCGGGCAGCCCACCTATCACCAACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
GCCCCATCCTTGCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
GGGTTCAGGATAGGGAATGGGGAGGTCAGAGGACGCAAAGCAGCAGCCATG**TAGA**ATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTTCGTATTTGGA
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

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FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVF PKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELRANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGP LESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

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FIGURE 152

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAAA
CTAAATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
TTCGATGGGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTGTGGCCATGTCCTTCCATT
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACTCAGGGCCAC
AGCCACCACCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCCTTTAGAGTGACAGGTAAAGCTGATACCAAAGGCTCCTGTGAGCACG
GTCTTGATCAAACTCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGT
GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCCTT
TTGCCAACAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
TCTTTTTGTTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT
GTCAGTAAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG
AATTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT
TGTTCTGTACTGATATTTAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF
HYDCGNKTVTPVSPLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTTCGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGA**ATG**GAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTGGGAGGCCAAC
CCACAGAACAGCATTCTGGGCCAGGCTG**TAA**TCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTCATTTTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGGQPTQHFWARL

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FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAG
 CTCTTGTGGCAGGTAAGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCC
 AGAACTGCCCCCTCCGTTTGCTCGTGCAGTAACAGTTCAGCAAGGTGGTGTGCACGCGCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGCAGT
 TGGGCAGGAACTCCATCCGGCAGATTGAGGTGGGGGCCTTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTTCGACAACCTGGCTGACAGTCATCCCTAGCGGGGCCTTTGAATACCTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCCTCTTACGCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTGATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAC
 CAACTTGGCCCAACAATAACCTCTCTTCTTTGCCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTGATGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCCACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCCACGTGCTGC
 TTTTACAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCCTA
 CCACGTCCACTGGTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTACAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGCGGAGTACAGTC
 ACAGCCGCCCCGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCACAATTC
 ATGACCATATTAACATAACACCTACAAACCAGCACATGGGGGCCACTGGACAGAAAAACAGC
 CTGGGGAACTCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTACAGACCA
 TACCAAGGACAAGGTACAGGAACTCAAATATGACTCCCTCCCCCAAAAACTTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTGTA
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATTTAAAGA
 CAAAAAGTCAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGLFNLKYLNLGMCNIKDMPNLTPLVGLEELEMNGHFPFIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAELNTSNYSFFTFTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTDKMQTSLDEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQORS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTE
NSLGNLHPTVTTISEPYIIQTHTKDKVQETQI

G E T A S

[illegible]

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAERNIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFGHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMPVQSRETPLH
QLYSAAFSKQKLQSAPTCKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDSSLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPEKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
AGCTTTCTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
TTCAACCTGACTTTCCACCTTTCCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCT
GACAGTGGTTGGGTGGGCCACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCCCTAAAG
CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACT
AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACTGTCCTTCTGTGTCTCCTTACCTCAG
AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC
CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
CTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
TTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC
TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
AACAACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACGAGTCTGG
AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
TATCAACATCACAGTGGATTTCTGGTTTGGTGCATGACCCTGGATCTTTTGGTGATGTTTGG
AAGAACTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCCTTTTTGTATTTTCTTAGCAGAGCT
CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG
AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
TATGGGATAAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCT
GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAG
CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTTAAAGAGTTTTTGTAAAATGA
TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAATA
TGTCTATCAAATACCTCTGTAGTAAATGTGAAAAAGCAAAA

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FIGURE 161

MGFNLT FHL SYKFRLLLLLTLC LT VVGWATS NYFVGAIQE I PKAKEFMAN FHKTL I LGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGV TALSREQFFKVNG
FSNNYWG WGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSV EHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCCGGGGTTCGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGCAGTTCTC
GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCCGCA**ATG**
GCCCAGGCAGTGTGGTTCGCGCCTCGGCCGCATCCTCTGGCTTGCCTGCCTCCTGCCCTGGGC
CCCGGCAGGGGTGGCCGCAGGCCTGTATGAACTCAATCTCACCACCGATAGCCCTGCCACCA
CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG
CCCGCTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGGCTTACTGGCAA
GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTTCGCCACGTGCCCCGGGAATTCCCGG
TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
GTCCTCCCCATCACAGAGTTCCCTCGTGGGGGACCTTGTGTGACCCAGAACACTTCCCTACC
CTGGCCCAGCTCCTATCTCACTAAGACCGTCTGAAAGTCTCCTTCCCTCCACGACCCGA
GCAACTTCCCTCAAGACCGCCTTGTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG
GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCACCGTGAAGCT
CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
CCGGGGACTTCTCCGCCTCGCTGAAGCTGCAGGAAACCTTTCGAGGCATCCAAGTGTGGGG
CCCACCCTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAAGTTCCTGGGGAGCCCTCC
TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCTCCCGCTGGAGGAAGGGGAGTGCCACC
CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCCCTGGGGACTAC
TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGA
TGTTGGCCTTCATCATGTACATGACCCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
AACCCGGAGCCACCCTCTGGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCCTTTCTTGCT
GGAGACTCCATCTGAGTACCTGGAAATTGTTTCGTGAGAACCACGGGCTGCTCCCGCCCCCTCT
ATAAGTCTGTCAAACTTACACCGTGT**AG**CACTCCCCCTCCCCACCCCATCTCAGTGTTAA
CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCAAT
TGCGTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTCAGCCACTGCCACAAGCC
CCTCCCTCTCTGTACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
TAAGCCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT
TTGATGCTTGGGGTGTTCGTGTTGACTCCTAGGTGGGCCTGGCTGCCCACTGCCCATTCCT
CTCATATTGGCACATCTGCTGTCCATTGGGGGTTCTCAGTTTCTCCCCAGACAGCCCTAC
CTGTGCCAGAGAGCTAGAAAGAAGGTATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACA
CACACACACACAGAAATATAAACACATGCGTCACATGGGCATTTTCAGATGATCAGCTCTGTA
TCTGGTTAAGTCGGTTGCTGGGATGCACCTGCCTAGAGCTGAAAGGAAATTTGACCTCCA
AGCAGCCCTGACAGGTTCTGGGCCCCGGGCCCTCCCTTTGTGCTTTGTCTCTCGAGTTCTTG
GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCCCTGGATGGGGGGCAGGACT
AATACTGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTG
AAACTTTCACTGAGGAAAAGGCCTTGACGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGG
TGGCTCACGCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA
GATCGAGACCACCCTGGCTAACACGGTGAACCCCGTCTCTACTAAAAAATACAAAAAGTT
AGCCGGGCGTGGTGGTGGTGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG
GTGCGAACCCGGGAGGCGGAGCTTGACGTGAGCCCAGATGGCGCCACTGCACTCCAGCCTGA
GTGACAGAGCGAGACTCTGTCTCCA

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FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLDVVTQNTSLPWPSSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFSSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCQMCCGPFLLETPEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

姓名	性别	出生年月	民族	籍贯	学历	学位	职称	工作单位	研究方向	主要成果	获奖情况	其他
王德胜	男	1965.10	汉族	山东烟台	本科		副教授	烟台大学	应用数学	《微分方程》	山东省教学成果奖	
李小明	男	1972.05	汉族	河南郑州	硕士	理学硕士	讲师	郑州大学	数学分析	《实变函数论》		
张小红	女	1978.12	汉族	江苏南京	本科		助教	南京理工大学	概率论	《概率论与数理统计》		
刘伟	男	1980.03	汉族	湖北武汉	硕士	理学硕士	讲师	武汉大学	统计学	《多元统计分析》		
陈丽	女	1985.08	汉族	浙江杭州	本科		助教	浙江大学	运筹学	《线性规划》		
赵国强	男	1960.11	汉族	四川成都	本科		副教授	四川大学	数学教育	《数学教育心理学》	四川省教学成果奖	
周建	男	1975.06	汉族	广东广州	硕士	理学硕士	讲师	中山大学	数学建模	《数学建模案例选编》		
吴昊	男	1982.01	汉族	安徽合肥	本科		助教	安徽大学	数学竞赛	《数学竞赛题选解》		
孙悦	女	1988.09	汉族	湖南长沙	本科		助教	湖南大学	数学教育	《数学教育心理学》		
马强	男	1970.04	汉族	陕西西安	硕士	理学硕士	讲师	西安交通大学	数学分析	《实变函数论》		
徐芳	女	1973.07	汉族	福建福州	本科		助教	福州大学	概率论	《概率论与数理统计》		
林峰	男	1977.10	汉族	江西九江	硕士	理学硕士	讲师	江西师范大学	统计学	《多元统计分析》		
黄娟	女	1983.02	汉族	广西桂林	本科		助教	广西大学	运筹学	《线性规划》		
郭亮	男	1979.05	汉族	云南昆明	硕士	理学硕士	讲师	云南大学	数学建模	《数学建模案例选编》		
何琳	女	1986.11	汉族	贵州贵阳	本科		助教	贵州大学	数学竞赛	《数学竞赛题选解》		
罗杰	男	1981.03	汉族	海南三亚	本科		助教	海南大学	数学教育	《数学教育心理学》		
宋佳	女	1989.06	汉族	宁夏银川	本科		助教	宁夏大学	数学分析	《实变函数论》		
李强	男	1974.09	汉族	新疆乌鲁木齐	硕士	理学硕士	讲师	新疆大学	概率论	《概率论与数理统计》		
王芳	女	1984.12	汉族	内蒙古呼和浩特	本科		助教	内蒙古大学	统计学	《多元统计分析》		
张磊	男	1976.04	汉族	吉林长春	硕士	理学硕士	讲师	吉林大学	运筹学	《线性规划》		
陈伟	男	1987.07	汉族	黑龙江哈尔滨	本科		助教	哈尔滨工业大学	数学建模	《数学建模案例选编》		
刘娜	女	1985.10	汉族	辽宁沈阳	本科		助教	沈阳理工大学	数学竞赛	《数学竞赛题选解》		
赵明	男	1971.01	汉族	山西太原	硕士	理学硕士	讲师	山西大学	数学教育	《数学教育心理学》		
吴昊	男	1982.05	汉族	河北石家庄	本科		助教	河北大学	数学分析	《实变函数论》		
孙悦	女	1988.08	汉族	河南郑州	本科		助教	郑州大学	概率论	《概率论与数理统计》		
马强	男	1970.11	汉族	山东烟台	硕士	理学硕士	讲师	烟台大学	统计学	《多元统计分析》		
徐芳	女	1973.02	汉族	江苏南京	本科		助教	南京理工大学	运筹学	《线性规划》		
林峰	男	1977.05	汉族	湖北武汉	硕士	理学硕士	讲师	武汉大学	数学建模	《数学建模案例选编》		
黄娟	女	1983.08	汉族	浙江杭州	本科		助教	浙江大学	数学竞赛	《数学竞赛题选解》		
郭亮	男	1979.11	汉族	安徽合肥	硕士	理学硕士	讲师	安徽大学	数学教育	《数学教育心理学》		
何琳	女	1986.04	汉族	湖南长沙	本科		助教	湖南大学	数学分析	《实变函数论》		
罗杰	男	1981.07	汉族	广西桂林	本科		助教	广西大学	概率论	《概率论与数理统计》		
宋佳	女	1989.10	汉族	云南昆明	本科		助教	云南大学	统计学	《多元统计分析》		
李强	男	1974.01	汉族	贵州贵阳	硕士	理学硕士	讲师	贵州大学	运筹学	《线性规划》		
王芳	女	1984.04	汉族	海南三亚	本科		助教	海南大学	数学建模	《数学建模案例选编》		
张磊	男	1976.07	汉族	宁夏银川	本科		助教	宁夏大学	数学竞赛	《数学竞赛题选解》		
陈伟	男	1987.10	汉族	新疆乌鲁木齐	本科		助教	新疆大学	数学教育	《数学教育心理学》		</

[illegible]

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FIGURE 165

MALSSQIWAACLLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCCHRSKCGMCCKT

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FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
CTGGATCTTCCACC**ATG**TTTCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
ATCTCCCTGACTGTCTCTTACCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG
AGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGCGGCTA
CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC
GGAATCATTGCAAAGGATCCCACCTTCACTAGAAGAAGAGATCAAAGAGATTCTGTCGAAGTGG
TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAAGTGG
GAGTCCTGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
GGTCCTGTGGGGGTTAGGAGTGCTGATTCTGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
TGGCTTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT
GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG
AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTCTAGAGAGCCATGGTGAAGGCCTG
CCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCCAGAAGGAACCTGCATC
AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC
TGTTGCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGA
TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAAATCTGC
CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGAGAAGG
TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA
AAGGACAGGAGCCGCTCC**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCCACTGCTGTGTCTTTCCAGACTCCAGGG
CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCGAGCCGCAGCGGGATCCCTGT
GCACCCGGCGCAGCCTACCCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
CGAGATGCCTTGTTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA
CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
GGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG
CTCTCCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGC
CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCATCTGCAGGGGCTTTCAGCAAAATG
AAGGGTTAGATTTTTATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTG
GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTTCGTACTCCAGGCTAACCTGAACTCCCC
ATGTGATGCGCGCTTTGTTGAATGTGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGG
GAATGGTGGTGATTCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGA
AGGACACATCACGTTTCAAGTACAGGCCCAAAAACGGGGCACGGCAGGCCTGAG
CTCAGAGCTGCTGCACTGGGCTTTGGATTTGTTCTTGTGAGTAAATAAAACTGGCTGTTGAA
TGA

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FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSEFGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRSKSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAEELSWNLLSRTNYNFQYISLRLTVLWGLGVLIRYCFLLPLRIALFTG
ISLLVVGTTVVGYPNGRFKEFMSKHVHLMCYRICVRAITAIITYHDRENRPNGGICVANH
TSPIDVILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQLYSKMIVGNHKDRSRS

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FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGGGATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCCAGGCTGTTCCACCATCCTGCCCCCTGGGCCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTA CTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCCGGGAGCTCTACATGAGGCACTTTCCTTCAAGGCCCTGCATTTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTTGGGCCCTGAAAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACCAGG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

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FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPPGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPPKALHFYLIRALQLLRSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLLLAPGEFQLSGVGP

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FIGURE 170

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATAACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCCCTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGGAACTCCTAACATATGCCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCACTCAC
TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAAATGTTATCTAGACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

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FIGURE 171

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEKKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

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FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCCTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCCTCCT
GTGTCTCCTGTTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAA
ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAA
AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCCTCCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAA**ATGA**AGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACATATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAT
TTTTTCATGAAATTATTCCTCTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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FIGURE 174

MKMLLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHG NFR LFLEQ
IHVLENSLV LKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQ LMGLYGREPD LSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTGAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTATAGGTCTATTGCT
TGTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAAAAA

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FIGURE 176

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATAGTGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNQLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTC
GAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

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FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPLITPGSATTC

FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCCC
TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCC
AGTGTTTCCACAGCCCCCAAACGGAACTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT
ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGGCCACCTATTTCCAGGGCTTTACGGT
ATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG
CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
GCCCCCTTCCATTTCAACATCCTGAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACA
TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
TCAGGAGAGGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA
GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGC
TTCCACAGGGCCTGCCGCCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTCG
CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
CTGGGTCTGTACAACCTTGGCAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
AAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCCC
TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCCG
ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
TCATCGATATTATAGGGGTCCATCACAACCCAACCTGTGTGGCCGGATCCTGAGGTCTACGAC
CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCTTTCTC
CGCAGGGCCCAGGAACGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCTCTGG
CGTTGATGCTGCTGCACTTCCGGTTCTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCA
TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCA
GTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPPQPPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGE GILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMEFHHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDAVIRERRRTLPTQGIDDFKDKAKSKTLD FIDVLLLSKDEG
KALSDEDI RAEADTFMFGGHD TTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

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FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTTAACCCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTCTGAAGTGAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCCTGTTTATTGTTACCTGGAAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAAAAA

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FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLDSREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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FIGURE 185

GAACATTTT TAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTT CAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAG**TGA**TCGCCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACGTGA

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FIGURE 186

MPSPGTVCSTLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC
GTGAACCCCGGGGTGCTCCGCACGGACCCCAAGATGTCAAGAATATGAACACGTGGCTGCTGT
TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
CTCCTGCTGGACTTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
GAGTATGTCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
GTCCCCCGTGTGCGCATGTGTTTCAAGGTGAGCCTCTCCAGAAAGTGAGATCATGGACAAAAA
GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCCCAGCAAGAAGCTGAAC
TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAAAATGTTTCA
GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
CCAAAAACACAAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTACCCACTAACCA
AACAACCTGAAGCGAGAGCTGTGGTCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT
AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
AACAACAACCTCCCTGCTCCTGGCACCAGCCGTTTTGGTTCATGGTGGGCCAGCTGCAAAGCG
TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
ACCCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
GCATCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA
GCCTCCTTGTTCATAACCACAGGTTACCCTACAAACCACTGTCCCCACACAACCCTGGGGAT
GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA
ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLS PRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAEELTPRPAGVVPGA

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FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAG
ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
TGCCCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACTGGGAGACTGGGGATGA
CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
AACCAGGGGAGAGGTGCCGAAGTTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAA
GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAA
GCGGTTGATGGAGAAGGCTTCCCTCCCCCTCCCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
TGTTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT
ACTAACAGACTTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAAGTGAAGCGCCTTTGCTG
CTGTTTCCTCTGTCCTGTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTC
TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAAATTATGGCTG
GGCCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCACCACCTTCA
ACACGTACACCAGGATGGTGTGGAGTTCAAGTGCAAGCA**TAG**TAAGAGCTTCAAGGAAAAC
CCGAAGTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCCAC
CGTGGGTCCCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA
GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
TCTCTTGAGCATGGTTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
CTAAGGGATTCCCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCACCCAC
CCCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTGGGC
TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNTSTQEVVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLETTCL
LWLGLLHGLALLHLLHGVGCHHLQHVVHVDGAGVQVQA

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FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTTGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCCTCTTCCTATTCTGTTCATCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTGAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCCGCCGTAGATTGAG
GACATTGCCCCCTGTGTGCCACCAAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT
ATGGCGATGGCCATGATGTTACAATCCCCTTGCCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCCTGAGGAAAAACCAAA
GGGAAGCAACAGGAACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

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FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQLACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

FIGURE 193

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCGTGGAGCCAGGAGCGACGTCA
 CCGCCATGGCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTGATGCTT
 GGATGTGCCCTTCCAATATACAACAAATACTGGCCCTCTTTGTTCTATTTTTTTTACATCCTTTCACCTATTCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAGGAACTTGCCATCTTTC
 TTACAACGGGCATTGTCGTGTGAGCTTTTGGACTCCCTATTGTATTGGCCAGAGCACATCTGATTGAGTGGGGA
 GCTTGTGCACTTGTCTCACAGGAAACACAGTCATCTTGAACATACTAGGCTTTTTCTTGGTCTTTGGAAG
 CAATGACGACTTCAGCTGGCAGCAGTGGTGAAGAAATTAAGTAATGTCAAATGGACTTCCTGTCAATTT
 GTTGGCCATTACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTTCACAGAGACTTGTGAAGGATTTAAAGGATTTTCT
 CTTTTGGAAAAGCTTGACTGATTTTACACTTATCTATAGTATGCTTTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTATGTGTTTTTCTGTAGGTTGATTTTTTTTTTGAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTTGCATTGGTTAGGAATTCAGAATTCGCCGCTCTATTACTGGTCAAGTACATCTTTCTCTTAAATTTATT
 TAGCCTCCATTATTACAAAAATTATAAAAAATAAGTTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACTGTTATAGACTGTATACTCAGTGCAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAGTGTAAATGCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG
 AAAATTATTTTATGGAATTGCTACAGAGGAGTGCTTTTCTTCTCAATTGTTAGAAGAATTTATGTTAAACTTTA
 AGGTAAGGGTGTAAAAACATTTTTGAGATAAGGTTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGT
 GGAAGAAATGACATTGAAATTCAGTTTTTGAATCCTGTTTCTATTTATAAGTGAATTTGTGATCTCCTATC
 AACCTTTCATGTTTTACCCTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCTCTTTGACTTATTTGGTATGTTGTATATATTACATAAAA
 TAACCTTTTCAAATATAGTTTAAATAACACTTAGAAGTGTTTACTTACCTGGAAAATAATTGCTATGCCGTACATT
 CAGAGTGCCCCCTCCCCTGCAAGGCCCTTGCCATGATTAACAAGTAACCTTGTAGTCTTACAGATAATTCATGCA
 TTAACAGTTTTAAGATTTAGACCATGGTAATAGTAGTTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAG
 TATTTTTAAGACAAGTTTCTGTATACCTCTGAAGTGTGTTTTGATTTTGTAGTTCATCATGATAGATCTGCTGTTT
 CCTTATAAAAGGCATTTGTTGTGTGAGTTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAAATCCCAGTAACCAGGCATGATCAATTTATAGTGGTCTGTTTACATCTAATAATTATCAGGA
 CTTTTTTCAGGAGTGGGTTATAAAAAACATTCAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTTGTATG
 TTTATTCAGTATACTTACATAAAAAATTTTCGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGT
 TTTATGAAGTTTATTTCTCAAGAAAATGGGAATAAATTTGGGATTTGTTTCTGCTTTTTTACTAAAGATGCCTAA
 AGCCACAGGTTTTATTGCCTAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCG
 GCGTGTGGCTGGAGCCTTCCCACTGGAGGCTGAAAGTGGCTTGTGGTATTATAATGTTTCAAGAGGAA
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTGTGCTTGTGATCTACTGGACTTT
 TTTTTTGCAGGAAGTGCATTCTCTGGTCTTCCCTATTTTCTGTTCTGGATGTCAGTGCAGTGCAGTGCAGTGCAGTGC
 TTTTATCCACTTGGCCACAGACTTTTTCTAACAGCTGCGTATTATTTCTATATACTAATGCAATGGCAGCATT
 GTGTCTTTGACCTTGATACTAGCTTGACATAGTGTCTGTCTGATTTCTAGGCTAGTTACTTGAGATATGAAT
 TTTCCATAGAATATGCACTGATACAACATTACCATTCTTCTATGGAAAAGAAAACCTTTTGATGATGAAACAATAA
 AGATTTTAAATATCTATTTTAAAAA

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FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

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[illegible]

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRLLISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRIILNSWKSITSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVAVYAFHLCEDGAEPTSG
HLLSAVTNRSDLGPPASSATTADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCCTCHQQPARECEV

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FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGGCGCCGTTGAGTTCCCGGCGGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTCTGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGGCCCTGGCGCTAG
CCCCGTGCGTGTCGCGAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGGCGTCCCGCGCGGGCCGCCTACGCTTCCACGGGCCGGGCGCGCTTGAGCGTG
GGCCCCGAGGACTGCGCGGACCCGTCTGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

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FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAUSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASERVGLGPGASPVVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

[illegible]

FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIP
FARDAVKKCFVCLA

FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGCGTTCCCTCCAGTCACCCTCCCGCCGTTACCCGCGGCGCGC
CCGAGGGAGTCTCCTCCAGACCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT
GGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACTACCATCCATAGCCAGATAGATTATCTTACACTG
AACTGATCAAGTACTTTGAAAATGACTTCGAAATTTATCTTGGTGTCTTCATACTTGCTGCACTGAGTCTTTC
AACCACCTTTTCTCTCCAAGTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACT
TATATAAAGTTCCAACGCCCCATTTTCATTATATTATGAAATATGGTGTTCACGTGAAGCAAGTTACTAATGTT
TTTATTACAAAAACCTACCCTAACCATTTACTTTGGTAACTGGCCTCTTTCAGAGAATCATGGGATTGTTGC
AAATGATATGTTTGATCCTATTGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCCAAGTTTT
GGGAAGAAGCGACACCAATATGGATCACAAACCAGAGGGCAGGACATACTAGTGGTGCAGCCATGTGGCCCCGA
ACAGATGTAAAAATACATAAGCGCTTTCCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAG
AGTTGCCAAAATTGTTGAATGGTTTACGTCAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCTG
ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCTTTTCAGATATTGACAAGAAGTTA
GGATATCTCATACAAATGCTGAAAAAGGCAAAGTTGTGGAACACTCTGAACCTAATCATCACAAGTGATCATGG
AATGACGCAGTGCTCTGAGGAAAGGTTAATAGAACTTGACCAGTACCTGGATAAAGACCCTATACCCTGATTG
ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAAGGTAATTTGATGAAGTCTATGAAGCACTAACTCACGCT
CATCCTAATCTTACTGTTTACAAAAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTCA
ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACATTTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACC
ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTCAGCCATGGTCTCTGCCTTCAGAAAGAATTTTC
TCAAAGAAGCCATGAACCTCCACAGATTTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
CAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
CTATACTCCTCCCTGGTAGTGTTAAACCAGCAGAATATGACCAAGAGGGGTCTATACCCTTATTTTCATAGGGGTC
TCTCTTGGCAGCATTATAGTGATTGTAATTTTGTAAATTTTCATTAAAGCATTTAATTCACAGTCAAATACCTGC
CTTACAAGATATGCATGCTGAAATAGCTCAACCATTATTACAAGCCCTAAATGTTACTTTGAAGTGGATTGTCATA
TTGAAGTGGAGATTCCATAATTATGTCAGTGTTTAAAGGTTTCAAATTTCTGGGAAACCAGTTCCAAACATCTGC
AGAAACCATTAAAGCAGTTACATATTTAGGTATACACACACACACACACACATACACACACACGGACCAAA
ATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGTCTCCATTGTTCACTGTAGCATAGGGATAGATAAG
ATCCTGCTTTATTTGGACTTGGCGCAGATAATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTATAT
ATTGCACTTTAAATTTCTCTCCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGTCTTATAAC
TTGATTGAAAATGACAACCTTTTGCACCCATGTACAGAATACTTGTTACGCATTGTTCAAACCTGAAGGAAATT
TCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAAGGTGATAAGTGTTGA
AAATTAATGTGATAACCTTTGAACCTTGAATTTTGGAGATGTATCCCAACAGCAGAATGCAACTGTGGGCAT
TTCTTGCTCTTATTTCTTCCAGAGAACGTGGTTTTTCATTTATTTTCCCTCAAAGAGAGTCAAATACTGACAG
ATTGTTCTAAATATATTGTTTCTGTATATAAATTTATTTGATTTTCTGATGAGTCATATTACTGTGATTTTCA
TAATAATGAAGACACCATGAATATACTTTTCTTCTATATAGTTCAGCAATGGCCTGAATAGAAGCAACCAGGCA
CCATCTCAGCAATGTTTTCTTGTGTTGTAATTTTGTCTCTTTGAAATTAATCACTATTAATTACATTAA
AAATCAAATTGATAAAAAAAAAAAAAAAAAAAAA

FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
ITNQ RAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAAGTGC GGGAGGCCAG
GACAGGCCACCCCTGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGC
AGAGAGGCCAAGCCCCTTGCCCTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACCTCACGGTCGTGGGAGACGA
CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG
AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC
CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
CAGCTCCACAGGTTTTAGGTCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCCGACAAGAATAACTATGCTGCCATG
GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
ATTTGTCTTCCGCCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
TGGTCTCATTATCCTGGACATTGTCCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAAACAGATGAATGTACAATTGGCCGCCA
AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCCTGGACTGATGAGTTTGCTGTATC
AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
CACACAGCCACCGTGAAAGTCCTGGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACC
AAAATCTATAAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEEEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSSHRFQVIIICLVVLDALLVLAELILD
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLLRLKQMNVLAAKIQHLEFS
CSEKPLD

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FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCGCCAACAT
 GCTCTGTCTGTGCCTGTACGTGCCGGTCATCGGGGAAGCCAGACCGAGTTCAGTACTTTG
 AGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCCTCC
 CAGGAATTCTCCACCTACCGCCAGTGGGAAGCAGAAAATTGTACAAGCTGGAGATAAGGACCT
 TGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGA
 GGCTGGTGTTTAAGATTTTGGACAAAAAGAATGATGGACGCATTGACGCGCAGGAGATCATG
 CAGTCCCTGCCGGACTTGGGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTCTCAAGAG
 CATGGATAAAAAACGGCACGATGACCATCGACTGGAACGAGTGGAGAGACTACCACCTCCTCC
 ACCCCGTGGAAAAATCCTCCGAGATCATCTCTACTGGAAGCATTCACAGATCTTTGATGTG
 GGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCAGACGGGGATGTGGTG
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCCCCCTGG
 ACAGGCTCAAGGTGCTCATGCAGGTCCATGCCTCCCGCAGCAACAACATGGGCATCGTTGGT
 GGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGGTCACTCTGGCGGGCAATGGCAGCA
 CGTCCCTCAAAATTGCCCCCGAATCAGCCATCAAAATTCATGGCCTATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACCAGGAGACTCTGAGGATTACGAGAGGCTTGTGGCAGGGTCTTTGGCA
 GGGGCCATCGCCAGAGCAGCATCTACCCAATGGAGGTCTGAAGACCCGGATGGCGCTGCG
 GAAGACAGGCCAGTACTCAGGAATGCTGGACTGCGCCAGGAGGATCCTGGCCAGAGAGGGGG
 TGGCCGCTTCTACAAAGGCTATGTCCCAACATGCTGGGCATCATCCCCTATGCCGGCATC
 GACCTTGCACTACGAGAGCCTCAAGAATGCTGGCTGCAGCACTATGCAGTGAACAGCGC
 GGACCCCGCGTGTTTGTGCTCCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGG
 CCAGCTACCCCTGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTCTATTGAGGGCGCT
 CCGGAGGTGACCATGAGCAGCCTCTTCAACATATCCTGCGGACCGAGGGGGCCTTCGGGCT
 GTACAGGGGGCTGGCCCCAATTCATGAAGGTGATCCAGCTGTGAGCATCAGCTACCTGG
 TCTACGAGAACCTGAAGATCACCTGGCGGTGAGTCCGCGGTGAAGGGGGAGGGCCGCCCG
 GCAGTGGACTCGCTGATCCTGGGCCGAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATG
 TGCCAACACTAAGCTGTCTCGAGCCAAGCTGTGAAAACCCCTAGACGCACCCGCAGGGAGGGT
 GGGGAGAGCTGGCAGGCCAGGGCTTGTCTGCTGACCCAGCAGACCCCTCCTGTTGGTTCC
 AGCGAAGACCACAGGCATTCCTTAGGGTCCAGGGTCCAGGCTCCGGGCTCACATGTGTAA
 GGACAGGACATTTTCTGCAGTGCCTGCCAATAGTGAGCTTGGAGCCTGGAGGCCGGCTTAGT
 TCTTCCATTTTACCCTTGCAGCCAGCTGTTGGCCACGGCCCCCTGCCCTCTGGTCTGCCGTGC
 ATCTCCCTGTGCCCTCTTGCTGCCTGCCTGTCTGCTGAGGTAAGGTGGGAGGAGGGCTACAG
 CCCACATCCCACCCCTCGTCCAATCCCATAATCCATGATGAAAGGTGAGGTACGTGGCCT
 CCCAGGCCTGACTTCCCAACCTACAGCATTGACGCCAATTTGGCTGTGAAGGAAGAGGAAAG
 GATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATGCT
 TGGGAGTGCAGGGGGCTCGGGCTGCCTGGCCTGGCTGCACAGAAGGCAAGTGTGGGGCTCA
 TGGTGTCTGAGCTGGCCTGGACCCTGTGAGGATGGGCCCCACCTCAGAACCAAACTCACTG
 TCCCCACTGTGGCATGAGGGCAGTGGAGCACCATGTTTGGAGGGCGAAGGGCAGAGCGTTTGT
 GTGTTCTGGGGAGGGAAGGAAAAGGTGTTGGAGGCCCTTAATTATGGACTGTTGGGAAAAGGG
 TTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTTCCTGTCCAACC
 CCAGCAGGGGGCGCAGCGGGACCGCCACATTCACCTTGTGTCACTGCTTGGAACTATTT
 ATTTTGTATTTATTTGAACAGAGTTATGTCCTAACTATTTTATAGATTTGTTTAAATTAATA
 GCTTGTCATTTTCAAGTTCATTTTTTATTCATATTTATGTTTCAAGGAGTGTACCTTCCC
 AAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGGCCTTGGGCCGCTGCAGTCACAT
 CTGTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAAGGCAGCAGCCCTG
 GCTCCTTTCTTTGGCAGGTTGGGGAAGGGCTTGGCCCCAGCCTTAGGATTTTCAAGGGTTTGA
 CTGGGGGCGTGGAGAGAGAGGGAGGAACCTCAATAACCTTGAAGGTGGAATCCAGTTATTTCT
 CTGCGCTGCGAGGGTTTCTTTATTTTCACTCTTTTCTGAATGTCAAGGCAGTGAAGTGCCTCT
 CACTGTGAATTTGTGGTGGGCGGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCCGTCCCTCC
 CAGCCTTCTGCTGCCCTTGCTTAACAATGCCGGCCAAGTGGCGACCTCACGGTTGCACTTCC
 ATTCCACCAGAATGACCTGATGAGGAAATCTTCAATAGGATGCAAGATCAATGCAAAAAATT
 GTTATATATGAACATATAACTGGAGTCGTCAAAAAGCAAAATTAAGAAAGAATTGGACGTTAG
 AAGTTGTCAATTAAGCAGCCTTCTAATAAAGTTGTTTCAAAAGCTGAAAAAAGAAAAA
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FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRLKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIKFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIIPYAGIDLAVYETLKNAWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
CAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTC
GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCÁCTTTTGAACCTGACATCAA
ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
AAGAAGGCCAAAGATGAGCTGTGGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTT
GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
AAACTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
CGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCA
GGGAGCCAACCTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA
TGAAGGTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGGCGGAG
TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTCTTTGCCATCAGCT
GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAATGTGCCTTGGCCACAAAAAAG
CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA
AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTGAAGTGTGTTAAGAGTGATAAG
TAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT
GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
TAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCA
CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
GGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT
TGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAA
AA

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FIGURE 208

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFQPTVVWASQVD
QGANFSEVSNTSFELNSENVMTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESEIKRR
SHLQLLSKASLCVSSFFAISWALLPLSPYLMLK

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[illegible]

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FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCSSLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVVRKTEAGVWD

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FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT
TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
TTGCTGGTATCACTGCAGTGCTTGTTGCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
GCTGAAGAACACTTTTCATTTTGTAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTTATG
AATCTAATGGAACCTCCTGTGCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTC
TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC
CAACGTCAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAACAAGACTCTTGGAGGAGTCA
TCTTTCGAAAGTTTGAGTGTGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT
TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
GGGACTGCTGCCCCTGAGGTCCTGGGGCTGCACTTTGCCAGCACCCCATTTCTGCTTCTCTG
AGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTCCCTGCTCTGCCCCGTTTAACTGC
CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA
AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLETPVR
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFEKANVNSLTPTSAPTTSNHNVGSKASLYLLALASLLLRGLLP

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FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
GGGCTTGCCTCACTGGCCACCCTCCCAACCCCAAGAGCCCAGCCCC**ATG**GTCCCCGCCGCCG
GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGGCGGGGGGGCCCAAGGCCTG
ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGGCCCCATGACCCGCAG
CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCCTCACCCACAG
CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCCGTGGCACTGCCAC
TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGCGCCT
TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTTGACCTATCAACAATGTC
CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
GCCTCTCAGAGCACCACCAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCAGCCCTGGCTTTTTGGAAACGGGTCA
GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
GACAGAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAAACCTGGAAAA
CACAA

FIGURE 214

MVPAAGALLWVLLLNLGPRAAGAQGLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAELLAATVSTGFSSRSAINEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMWPWGPWHCHCKSGTMSRSRSGKLGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSCTDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA
FWKRVIRIGLEDIWNSLSSVFTEMQPIDRNQR

FIGURE 215

CCCCGGTTCGACCCACGCGTCCGGGGAGAAAGGATGCGCGGCTGGCGGCGCGGTTGGTCTGCTAGCTGGGGCA
GCGGCGCTGGCGAGCGGCTCCAGGGCGACCGTGAGCCGGTGTACCGCGACTGCGTACTGCAGTGCGAAGAGCA
GAACTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT
GTCGGGACGACTGTAAGTATGAGTGTATGTGGGTCAACGTTGGGCTCTACCTCCAGGAAGGTCAAAAGTGCCT
CAGTTCCATGGCAAGTGGCCCTTCTCCCGGTTCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCCTCGTTTTCT
CAATGGCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCATGTACCACA
CCTGTGTGGCCTTCGCCTGGGTGCCCTCAATGCATGGTCTGGTCCACAGTCTTCCACACCAGGGACACTGAC
CTCACAGAGAAAATGGACTACTTCTGTGCCTCCACTGTCATCCTACACTCAATCTACCTGTGCTGCGTCAGGAC
CGTGGGGCTGCAGCACCCAGCTGTGGTCAGTGCCTTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCT
CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTG
GTGTGGTGGCTGGCCTGGTGCTGTGGAACCAGCGGCGGCTGCCTCACGTGCGCAAGTGCGTGGTGGTGGTCTT
GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCCACCGCTCTTCTGGGTCTGGATGCCCATGCCA
TCTGGCACATCAGCACCATCCCTGTCCACGTCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG
AAGGAATCAGAGGACAAGTTCAAGCTGGACTGAAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCC
GCCCCTGCTGGCCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAAGTTGGACATGA
AGGATGTGGGCCAGAAATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG
AAGGCCTCCAGCATCTGGGACTCGAGAGTGGGAGCCCTCTACCTCCTGGAGCTGAAGTGGGGTGGAACTGA
GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCTGTTTCTCCACCAGCCTCCTCCACATCCCCAGCTG
CCTGGCTGGGTCTGAAGCCCTCTGTCTACCTGGGAGACCAGGGACCACAGGCCTTAGGGATACAGGGGTCCC
CTTCTGTTACCACCCCCACCTCCTCCAGGACACCACTAGGTGGTGTGCTGGATGCTTGTCTTTGGCCAGCCAA
GGTTCACGGCGATTCTCCCCATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTACCCCTGACC
GTTGCCCTAGCCAGGTTCCAGGAGGCCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCCAGGGCA
AGGATCCTGTGCTGCTGTGTTGAGAGCCTGCCACCGTGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGG
TGACAGGGCCGTGAGCATGGCCCTGGGTGTGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTTGT
CGGGGAAGAGGTGTGGCTTCAAAGTGTGTGTGTGCGAGGGGGTGGGTGTGTTAGCGTGGGTTAGGGGAACGTGTG
TGCGCGTGCTGGTGGGCATGTGAGATGAGTGACTGCCGGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT
GAGGGAATCCTGTCAACATCAATAATCACTTGTGGAGCGCCAGCTCTGCCCAGACGCCACCTGGGCGGACAGC
CAGGAGCTCTCCATGGCCAGGCTGCCTGTGTGATGTTCCCTGTCTGGTGCCCCCTTGGCCGCTCCTGCAAC
CTCACAGGGTCCCCACACAACAGTGCCTCCAGAAGCAGCCCTCGGAGGCAGAGGAAGGAAAATGGGGATGGC
TGGGGCTCTCTCCATCCTCCTTTTCTCCTTGCCTTCGCATGGCTGGCCTTCCCCTCCAAAACCTCCATTTCCCT
GCTGCCAGCCCCCTTGGCATAGCCTGATTTTGGGGAGGAGGAAGGGGCGATTGAGGGAGAAGGGGAGAAAGCT
TATGGCTGGGTCTGGTTTCTTCCCTTCCCAGAGGGTCTTACTGTTCCAGGGTGGCCCCAGGGCAGGCAGGGGCC
ACACTATGCCTGTGCCCTGGTAAAGGTGACCCCTGCCATTTACCAGCAGCCCTGGCATGTTCTGCCCCACAGG
AATAGAATGGAGGGAGCTCCAGAACTTTCCATCCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTTG
CTCTGCCCTGACCCCTTGTCCCTCTTTGAGGGAGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTG
GCCTGCGCTAGCTTCTTTTGATACTGAAAACCTTTTAAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAA
TTCCAAGCCTCAAAAAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAWFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLQLGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEHEEL
DAEVLEVFPHTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLOYEDKFRNNLKGKRLDINTN
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
RLINKFNSSSSSLEEKIAALFDLEYVHQMDNAQDLLSFQGLQVVINGLNSTEPLVKEYAAF
VLGAASFSSNPQVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
GGLQVLRRTLQVEKGTEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKLQOYRQVHLLPG
LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

[illegible]

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FIGURE 220

MGA AVFFGCTF VAFGPAFALFLITVAGDPLRV IILVAGAFFWLVSLLLASV VWFILVHVTD R
SDARLQYGLLI FGA AVSVLLQE VFRFAYYKLLKKADEGLASLSE DGRSPISIRQMAYV SGLS
FGIISGVFSVINILADALGPGVVG IHG DSPYYFLTSAFLTA AIILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

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FIGURE 221

AAGCTGGTTTAAAGGAAGCAGAGGAGGGTTAGATTTCGTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCGTTCAGATGCCCCGGTTCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCCTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTCCTGTCCTGGTCAGGCCCCACCCCCCTTCCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTCGCGTTCGGCCCGGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCCCNTTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCCCTCCCATTTGCCTGTCCTGGTCAGGCCCCACCCCCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGGTTTCGGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTGAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG
TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
TGTCTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCCTCCTTGCCCTGTCTGGAGGCTGCT
AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCCGT
CCTTGTGGTTTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCC
CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
CTCGCCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
GGACCTGGGAGCTGGGGCCGGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA
ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCCACTGCAG
GAAGAAAGTTTTAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAGTTTATGAATCTGGGC
AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCTGGCTACTCCCACCCTGGCCACTCT
AACGACCTCATGCTCATCAAAGTGAACAGAAGAATTTCGTCCTCCACTAAAGATGTCAGACCCAT
CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
CCAAGAGCCCCCAAGTGCACCTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
TGCAGGGACTCGTGTCCTGGGGAGATTACCCTTGTGCCCCGGCCCAACAGACCGGGTGTCTAC
ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCAT
CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCAG
ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCT
CCTGGACTCAGGGTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGG
GAACAATTTCCAAAAGTGTCCAGGGCGGGGGTTCGCTCTCAATCTCCCTGGGGCACTTTTCAT
CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAA
CTGAGAAGTGGAATAAAAAA

FIGURE 226

MATARPPWMWVLCALITALLLGVTEHVLANNVSCDHPSENTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPHGYSHPGHSNDLMLIKLNRIRIPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGRDSCQGD SGGP
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCCAACTTGAGGACCGGCCGCGCGA
 CAAGCCGACGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGCTGCTGGCCCTGGGTGTGC
 TGCTGGCTGTAGCTGTACCGGTGCCGTGCTCTTCTGAACCACGCCCACGCGCCGGGCACG
 GCGCCCCACCTGTCTCAGCACTGGGGCTGCCAGCGCCAACAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACAGCTCGCACCTCAGCATCCTCATTGACCCGCGCTGCCCCGACCTCACCGACA
 GCTTCGCACGCCTGGAGAGCGCCAGGCCTCGGTGCTGCAGGCGCTGACAGAGCACCAGGCC
 CAGCCACGGCTGGTGGGCGACCAGGAGCAGGAGCTGCTGGACACGCTGGCCGACCAGCTGCC
 CCGGCTGCTGGCCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCATG
 GCACGCTGGGCCAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGGCCGCCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTGAGCGACATCCTGGATGCCCT
 GCAGAGGGACCGGGGGCTGGGCCGGCCCCGCAACAAGGCCGACCTTCAGAGAGCGCCTGCCC
 GGGGAACCCGGCCCCGGGGCTGTGCCACTGGTCTCCCGGCCCGAGACTGTCTGGACGTCCTC
 CTAAGCGGACAGCAGGACGATGGCGTCTACTGTCTTTCCACCCACTACCCGGCCGGCTT
 CCAGGTGTACTGTGACATGCGCACGGACGGCGCGGCTGGACGGTGTTCAGCGCCGGGAGG
 ACGGCTCCGTGAACTTCTTCCGGGGCTGGGACGCGTACCGAGACGGCTTTGGCAGGCTCACC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACGAGCT
 GCACGTGGACCTGGAGGACTTTGAGAATGGCAGGGCTATGCCCGCTACGGGAGCTTCGGCG
 TGGGCTTGTTCTCCGTGGACCCTGAGGAAGACGGGTACCCGCTCACCCTGGCTGACTATTCC
 GGCACCTGCAGGCGACTCCCTCCTGAAGCACAGCGGCATGAGGTTTACCACCAAGGACCGTGA
 CAGCGACCATTAGAGAACTGTGCCGCTTCTACCGCGGTGCCTGGTGGTACCGCAACT
 GCCACACGTCCAACCTCAATGGGCGAGTACCTGCGCGGTGCGCACGCCCTCCTATGCCGACGGC
 GTGGAGTGGTCTCTGGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 GCGGTCCCGGAGGACCGCT**TAG**ACTGGTGCACCTTGTCTTGGCCCTGCTGGTCCCTGTGCG
 CCCATCCCCGACCCACCTCACTCTTTCGTGAATGTTCTCCACCCACCTGTGCCTGGCGGAC
 CCACTCTCCAGTAGGGAGGGGCCGGGCCATCCCTGACACGAAGCTCCCTGGGCGGGTGAAGT
 CACACATCGCCTTCTCGCCGTCCCCACCCCTCCATTTGGCAGCTCACTGATCTCTTGCCCTC
 TGCTGATGGGGCTGGCAAACCTTGACGACCCCAACTCCTGCCTGCCCCACTGTGACTCCGG
 TGCTGTTTGGCGTCCCTGGCCAGGATGGTGGAGTCTGCCCCAGGCACCTCTGCCCTGCCC
 GGCCAAATACCCGGCATTATGGGGACAGAGAGCAGGGGGCAGACAGCACCCCTGGAGTCCTC
 CTAGCAGATCGTGGGAATGTGAGGTCTCTCTGAGGTGAGGTCTGAGGCCAGTATCCTCCAG
 CCTCCCAATGCCAACCCCAACCCGTTTCCCTGGTGCCCAGAGAACCCACCTCTCCCCCAA
 GGGCCTCAGCCTGGCTGTGGGCTGGGTGGCCCCATCCTACCAGGCCCTGAGGTGAGGATGGG
 GAGCTGCTGCCCTTGGGGACCCACGCTCCAAGGCTGAGACCAGTTCCTGGAGGCCACCCAC
 CCTGTGCCCCGGCAGGCCTGGGGTCTGCAGTCTCTTACCTGCTGTGCCACCTGCTCTCTG
 TCTCAAATGAGGCCCAACCCATCCCCACCCAGCTCCCGGCCGTCTCTACCTGGGGCAGC
 CGGGGCTGCCATCCCATTTCTCTGCTCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT
 GGACTGCGCTAATGGGAAGCTCTTGTTTTCTGGGCTGGGGCCTAGGCAGGGCTGGGATGAG
 GCTTGTAACAACCCCAACCAATTTCCCAAGGGACTCCAGGGTCTGAGGCCTCCAGGAGG
 GCCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCCATGAGGAGGCCAACCCTTGCC
 ATTGACCGTGGCCACCTGGACCCAGGCCAGGCCCGGCCGCGAGTGGTCAAGGGACAGGGA
 CCACCTCACCGGGCAAATGGGGTGGGGGGACTGGGGCACCAGACCAGGCACCACCTGGACA
 CTTTCTTGTTGAATCCTCCCAACCCAGCACGCTGTCATCCCCACTCCTTGTGTGCACACA
 TGCAGAGGTGAGACCCCGCAGGCTCCAGGACCAGCAGCCACAAGGGCAGGGCTGGAGCCGGG
 TCCTCAGCTGTCTGCTCAGCAGCCCTGGACCCGCGTGCGTTACGTCAGGCCCAGATGCAGGG
 CGGCTTTTCCAAGGCCTCCTGATGGGGGCCCTCCGAAAGGGCTGGAGTCAGCCTTGGGGAGCT
 GCCTAGCAGCCTCTCCTCGGGCAGGAGGGGAGGTGGCTTCTCCAAAGGACACCCGATGGCA
 GGTGCCCTAGGGGGTGTGGGGTTCCGTTCTCCCTTCCCTCCCACTGAAGTTTGTGCTTAAAA
 AACAATAAATTTGACTTGGCACCCTGGGGGTGGTGGGAGAGGCCGTGTGACCTGGCTCTC
 TGTCCCAGTGCCACCAGGTCATCCACATGCGCAG

FIGURE 228

MVNDRWKTMGGAAQLEDPRDPKQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQELLDTLADQLPRLLARASELQTECMGLRKHGHTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCCTGCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC
 TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAACTCTGTGCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTACCATGCTGAAGATAAACAAACAAGAAGA
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCAT
 GTCTTCCTTACACTTGGTGGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAAATACACAAGGAATCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCCATTAAGACTCTGATAATTG
 TCTCCCCTCCATAGGAATTTCTCCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTTCA
 GTACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDDGD TTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDN CYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT
GTGGCTGAAAACTCTGTCTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACACCACTTCCC

FIGURE 232

GCCGAGCGCAAGAACCCTGCGCAGCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCGGGG
 CCCGAGCCCTCCGGATCCGCCCCCTCCCCGGTCCCCGCCCTCGGAGACTCCTCTGGCTGCT
 CTGGGGGTTTCGCCGGGGCCCGGGACCCGCGGTCCGGGCGCC**ATG**CGGGCATCGCTGCTGCTG
 TCGGTGCTGCGGCCCCGAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTACCCTGAGCCT
 GCTCAGCGTCACCTGGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCCAACCTGGAGACTCTG
 AGCTGCCGCCGCGCGGCAACACCAACGCGGCGCGCCGGCCCAACTCGGTGCAGCCCCGAGCG
 GAGCGCGAGAAGCCCGGGGCGGGCGAAGGCGCCGGGGAGAATTGGGAGCCGCGCGTCTTGCC
 CTACCACCCTGCACAGCCCGGCCAGGCCGCCAAAAGGCCGTGAGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCCC
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTTCCTGAC
 GGGCGCACGGGGCCGCCGGGCCCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTTCTTCCTGGTGCCTGACACCACCTACACCGAGGCGCACGGCCTGGCACGCCTAACTGG
 CCACCTCAGCCTGGCCTCCGCCGCCACCTGTACCTGGGCCGGCCCCAGGACTTTCATCGGCG
 GAGAGCCACCCCGGCCGCTACTGCCACGGAGGCTTTGGGGTGTGCTGTGCGCGCATGCTG
 CTGCAACAACCTGCGCCCCACCTGGAAGGCTGCCGCAACGACATCGTCAGTGCGCGCCCTGA
 CGAGTGGCTGGGTGCTGCAATTCTCGATGCCACCGGGGTGGGCTGCACTGGTGACCACGAGG
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGGAGCCAGTGACAGGAGGGGGACCCTCAT
 TTCCGAAGTGCCCTGACAGCCACCCTGTGCGTGACCCCTGTGCACATGTACCAGCTGCACAA
 AGCTTTTCGCCCGAGCTGAACTGGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAATACCAGCCATCTGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATT
 CCAGCACCATCCCCGCCCGCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA
 GCACGCTTTCTCTGCGCCGATGGCTCACCCCGCTGCCACTGCGTGGGGCTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCCGGCCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCCGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCCAGGGAGGCGCCGGCCCCCTCACTC
 GCCGAGTGACGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCCTGTGCCCTATGTCACT
 GAGGCCCTCACGTCTCACTGTGCTGCTGCCTCTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGG
 CTTCTTGAGAGCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGGCCCATGCAGATGTCTTCGCACCT
 GTCAAGGCCACGTGGCAGAGCTGGAGCGGCGTTTCCCCGGTGCCCGGTGCCATGGCTCAG
 TGTGCAGACAGCCGCACCCTCACCACCTGCGCCTCATGGATCTACTCTCCAAGAAGCACCCGC
 TGGACACACTGTTCCCTGCTGGCCGGGCCAGACACGGTGCTCACGCCTGACTTCTGAACCGC
 TGCCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTTCCCATGCATTTCCAAGCCTTCCA
 CCCAGGTGTGGCCCCACCACAAGGGCCTGGGCCCCCAGAGCTGGGCCGTGACACTGGCCGCT
 TTGATCGCCAGGCAGCCAGCGAGGCCTGCTTCTACAACCTCCGACTACGTGGCAGCCCGTGGG
 CGCCTGGCGGCAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT
 GTTCCCTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGCAGCGCT
 ACCGGGCCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGTACCACCGCTGCCTCCAGAGC
 GTGCTTGAGGGCCTCGGCTCCCGAACCCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGGG
 CAACAGCACCT**TGA**CCCCACCCTGTCCCCGTGGGCCGTGGCATGGCCACACCCACCCCACTT
 CTCCCCAAAACCAGAGCCACCTGCCAGCCTCGCTGGGCAGGGCTGGCCGTAGCCAGACCCC
 AAGCTGGCCCCACTGGTCCCCTCTCTGGCTCTGTGGGTCCCTGGGCTCTGGACAAGCACTGGG
 GGACGTGCCCCCAGAGCCACCCACTTCTCATCCCAAACCCAGTTTCCCTGCCCCCTGACGCT
 GCTGATTCTGGGCTGTGGCCTCCACGTATTTATGCAGTACAGTCTGCCTGACGCCAGCCCTGC
 CTCTGGGCCCTGGGGGCTGGGCTGTAGAAGAGTTGTTGGGGAAGGAGGGAGCTGAGGAGGGG
 GCATCTCCCAACTTCTCCCTTTTGGACCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCA
 AGTGTGGAAAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELP
PRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRL
LVAVL
TSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRH
LLE
QHGDDEFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCH
GGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLDATGVGCTGDHEGVHYSHLELS
PGEP
VQEGDPHFERSALTAHPVRDPVHMYQLHKAFARAELEPTYQEIQELQWEIQNTSHLAVD
GDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLTAL
EELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPL
SRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTL
LLLYEPRQAQRVA
HADVFAPVKAHVAELEERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAG
PDTV
LTPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGPGPPELGRDTGRFDRQAASE
ACFYNS
DYVAARGRLAAASEQEEELLES
LDVYELFLHFSS
LHVLRAVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSRTQLAMLLFEQEQGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT
AGCTATTAGCCAATTCGGCAGGGCCCGCTTTTTAGAAAGCTTGATTTCCCTTTGAAGATGAAAG
ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA
CTGTATCCACCCAAATGTCACCGATTTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA
GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAG
AGGGTTGCTCAACGCCCCGCCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTG
GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
TTCCCCGCCCCCTGAGACCCTGCAGCACCATCTGT**ATG**GCGGCTGGGCTGTTTGGTTTGAGC
GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCCGCGTCCGCTGGGA
ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAAGCGGCCCCCAGAAC
CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCCA
GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGTCTGGAACATGCGACTTGTCTTCTT
CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTGTGGCCTATCTGCCTGACTACA
GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
CTTCCCATCATGGAATCCAACCTGCTTCGACCCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCCTGCCTGCCATTCTGAC
CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

FIGURE 235

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE
DENLYEKNPDSHGDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGGCCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAAC TTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAC TGCTTCGACCCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCCTGTTGCTCCTGGGGCCCCGGCGGCTGGTGCCT
TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACTTGTTCATCACCCCGCTGCCTTCCGGGG
ACGTAGCCCGCCACATTCCAGTTCCGCACGCGCTGGGATTCGGAGCTTCAGCGGGAAGGAGTG
TCCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
GCTGCACCTGTCATTACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCCTTCTGC
AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA
TCTTGGAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC
CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCTCTCTGTGCTGCTGAAGGCAGA
TCGCTTGTTCCACACCAGCTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGCAGAAATG
CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCAGTTGTATTTGATGCCTTC
ATCACGGGGCAGGGAAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTCACGGA
GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACAACCAGGACA
ACGAGACATTAGAGGTGCACCCACCCCCGACCACTACATATCAGGACGTCATCCTAGGCACT
CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
CAACATCCAGCTCAAGTGGAAGAGACCCCCAGAGAATGAGGCCCCCCCCAGTGCCCTTCTCTGC
ATGCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC
AACACCCACCCATACCGGGCCTTCCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCG
GCTGTATGTGCACACCCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
ACTACCAGCCTGCCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTACAGCTGCCG
GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
CACGCCAGATCCTAACCATGGCTTCTATGTACAGCCCATCTGTCCTCAGCGCCCTTGTGCCCA
GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCCTCTTCAACAGCCTGTTCCCA
GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT
GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
GGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCACTCT**TGAT**
CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT
TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTCAGGGC
CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGAATTTGAATTAA
CTTAGAAATTCATTTCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTTCCATCACACAGAAAGGTC
GGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGGA
TGGAGTTTACTGTTTGTGGAATAAAAACGGCTGTTTCCGTGGAAAAA

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FIGURE 238

MPLALLVLLLLGPGGWCLAEPDRSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDTVTDVDKSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSSISWELRQTLSVVFDAFITG
QGKKDWSLFRMFSTRTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLPDPFSMPYNVICLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTCACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAACTGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCCTCAGAATGATGCTGGGTCCTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAAG
TCCAGACCCCAGGGACGGTACTTTCCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGGACTTCCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

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FIGURE 240

MGSSSFVLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEKGKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACTCAGCACTTGCCGGAGTGGCTCATTTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGG
AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
TCTAGAACCCGACCCACCACC**ATG**AGGTCTGCCTGTGGAGATGCAGGCACCTGAGCCAAGG
CGTCCAGTGGTCCTTGCTTCTGGCTGTCTGGTCTTCTTTCTCTTCGCCTTGCCCTCTTTTA
TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGCCCAAGGCCCACACCA
CCGGAGACAGAGGAAAGGAGGGCAACCAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC
ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAAACCATGGTGAACACACTGTC
ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
AGGACACAAAGACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
GTGTCAGAGAAGCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTTCCAAAAGTCA
GCACAGAATGCTGGCTCCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
CAGCAGTCATCCCACCTAAGGAGAAGAAACCTCAGGCCACCCCAACCCCTGCCCTTTCCAG
AGCCCCACGACGCAGAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
GGATTTTGAGGAAAAATACAGCTTCGAAATAGGAGGCCCTTCAGACGACTTGCCCTGACTCTG
TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCCAACCTCACTCTC
TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCTGGAACACTTTGCACCACC
CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCTCCAG
TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGT
GCCGTGGTGGGCAACGGGGGCATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA
CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAGGCTACGAACAGGATGTGGGGACTC
GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT
CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACTTCCTGGAAGGCAC
CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
TCTGGTTTCAGGCACAGACCCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCTGGA
TGGTGGCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC
AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGTCCTGGTC
CCGGAAGTGCCAAAGCCAAGAAC**TGA**CCGGGGCCAGGGCTGCCATGGTCTCCTTGCTGCTC
CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA
GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
GGCAAATGGCTAATTGAGGTTCTGAAGTTCTTCAGTACATTGCTGTAGGTCTGAGGCCAGG
GATTTTAAATTAAATGGGGTGATGGGTGGCCAATACCACAATTCCTGCTGAAAAACACTCTT
CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTTACAGAAACATATAGATCTG
GTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTTCACTAC
AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGGTCTATACTTGTCTTG
TCTTTAAGCTATTTGACAACCTCTACGTGTTGTAGAAAACTGATAATAACAAATGATTGTT
GTCCATGGAAAGGCAAATAAATTTTCTACAGTGAAAAA

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHRQRTENIKERSLQSLAKP
KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKLTASRTVSEKHQG
KAATTAKTLIPKSQHRMLAPTGAVSTRTRQKGVTTAVIPPKEKKPQATPPAPFQSPPTQORN
QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHF
NQSEWDRLEHFAPPPFGFMELNYSLVQKVVTFRFPVPQQQLLLASLPAGSLRCITCAVVGNGG
ILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATAFSLTQSLILGNRGFKNVP
LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLLHPDFL
RYMKNRFLRSKTLGDGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

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FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTGCAGACAGACTCTTCATAAGTCCTTTGAGTTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

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FIGURE 244

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

FIGURE 245

GGGCTGGGCCCCGCCGCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
CCCGACCCCGGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGCGCCG
CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGACTGCCT
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCCCTGTTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGACCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA
ACTATGAGGGGTGGGGGGAGGGCTTGGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG
GAGATGACAGCCTGGGTCACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAAGACAAAA

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FIGURE 246

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGGCGGCGCAAGGGTGAGGGCGGCCCCAGAA
 CCCAGGTAGGTAGAGCAAGAAG**ATG**GTGTTTCTGCCCCCTCAAATGGTCCCTTGCAACCATG
 TCATTTCTACTTTTCCTCACTGTTGGCTCTCTTAACTGTGTCCACTCCCTTCATGGTGTGAGAG
 CACTGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCTTTGGAATAAAATACGACTTC
 CTGAGTACGTCATCCCAGTTCATTATGATCTCTTGATCCATGCAAACCTTACCACGCTGACC
 TTCTGGGGAAACCACGAAAGTAGAAATCACAGCCAGTCAGCCCACCAGCACCATCATCCTGCA
 TAGTCACCACCTGCAGATATCTAGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGG
 AAGAACCCTGCAGGTCTGGAACACCCCCCTCAGGAGCAAATTGCACTGCTGGCTCCCGAG
 CCCCTCCTTGTGGGCTCCCGTACACAGTTGTCTTCACTATGCTGGCAATCTTTGCGAGAC
 TTTCCACGGATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAACCTGAGGATACTAGCAT
 CAACACAATTTGAACCCACTGCAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTC
 AAAGCAAGTTTCTCAATCAAATTAGAAGAGAGCCAAGGCACCTAGCCATCTCCAATATGCC
 ATTGGTGAAATCTGTGACTGTTGCTGAAGGACTATAGAAGACCATTTTGTATGTCACTGTGA
 AGATGAGCACCTATCTGGTGGCCTTCATCATTTTCAAGTTTGTAGTCTGTGAGCAAGATAACC
 AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGC
 ACTGGATGCTGCGGTGACTCTTCTAGAATTTTATGAGGATTATTTTCAAGCATACCGTATCCCC
 TACCCAAACAAGATCTTGCTGCTATTTCCGACTTTTCACTGCTGGTGCTATGGAACCTGGGGA
 CTACACAACATATAGAGAATCTGCTCTGTTGTTTATGATGCAGAAAAGTCTTCTGCATCAAGTAA
 GCTTGGCATCACAGTGACTGTGGCCCATGAACTGGCCACCAGTGGTGTGGGAACCTGGTCA
 CTATGGAATGGTGGAATGATCTTTGGCTAAATGAAGGATTGCCAAATTTATGGAGTTTGTG
 TCTGTGAGTGTGACCCATCCTGAACTGAAAGTTGGAGATTATTTCTTTGGCAAATGTTTTGA
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCCTGTGTCTACACCTGTGGAAAATCCTG
 CTCAGATCCGGGAGATGTTTGTATGATGTTTCTTATGATAAGGGAGCTTGTATTCTGAATATG
 CTAAGGGAGTATCTTAGCGCTGACGCATTTAAAGTGGTATTGTACAGTATCTCCAGAAGCA
 TAGCTATAAAAATACAAAAACGAGGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAG
 ATGGTGTAAGGGGATGGATGGCTTTTGGCTCTAGAAGTCAACATTCATCTTCATCCTCACAT
 TGGCATCAGGAAGGGGTGGATGTGAAAACCATGATGAACACTTGGACACTGCAGAGGGGTTT
 TCCCTAATAACCATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA
 AGGGCTCTGACGGCGCCCCGGACACTGGGTACCTGTGGCATGTTCCATTGACATTATCACC
 AGCAAATCCAACATGGTCCATCGATTTTTGCTAAAAACAAAAACAGATGTGCTCATCCTCCC
 AGAAGAGGTGGAATGGATCAAATTTAATGTGGGCATGAATGGCTATTACATTGTGCATTACG
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAGGAACACACACAGCAGTCAGCAGT
 AATGATCGGGCAAGTCTCTAACAATGTCATTTTCACTCGTCAAGCATTGGGAAGCTGTCCAT
 TGAAAAGGCCTTGGATTTATCCCTGTACTTGAAACATGAACTGAAATTATGCCCGTGTTC
 AAGGTTTGAATGAGCTGATTCCATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGTG
 GAACTCAATTCAAGGCCTTCCCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG
 GACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCGGAGTGAACACTACTCCTCGCCTGTG
 TGCACAACATATCAGCCGTGCGTACAGAGGGCAGAAGGCTATTTTCAAGAAAGTGAAGGAATCC
 AATGGAAACTTGAGCCTGCCTGTGACAGTGACCTTGGCAGTGTGTGCTGTGGGGGCCAGAG
 CACAGAAGGCTGGGATTTTCTTTATAGTAAATATCAGTTTTCTTTGTCCAGTACTGAGAAAA
 GCCAAATTGAATTTGCCCTCTGCAGAACCCAAAATAAGGAAAAGCTTCAATGGCTACTAGAT
 GAAAGCTTTAAGGGAGATAAAAATAAAACTCAGGAGTTTCCACAAATTCTTACACTCATTGG
 CAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAGGAAAAACTGGAACAACTTG
 TACAAAAGTTTGAACCTGGCTCATCTTCCATAGCCACATGGTAATGGGTACAACAAATCAA
 TTCTCCACAAGAACACGGCTTGAAGAGGTAAAGGATTCTTCAGCTCTTTGAAAGAAAATGG
 TTCTCAGCTCCGTTGTGTCCAACAGACAATTGAAACCATTGAAGAAAACATCGTTGGATGG
 ATAAGAATTTTGATAAAATCAGAGTGTGGCTGCAAAGTGAAAAGCTTGAACGTATG**TAAAA**
 TTCTCCCTTGCCCGGTTCTGTTATCTTAATCACCACATTTTGTGTGAGTGTATTTTCAA
 ACTAGAGATGGCTGTTTTGGCTCCAACCTGGAGATACTTTTTTCCCTTCACTCATTTTTTGA
 CTATCCCTGTGAAAAGAATAGCTGTTAGTTTTTTCATGAATGGGCTTTTTTCATGAATGGGCTA
 TCGCTACCATGTGTTTTGTTTCATCACAGGTGTTGCCCTGCAACGTAAACCCAAGTGTGGGT
 TCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLOVLE
HPPQEQIALLAPEPLLVLGPLYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
ARMAFPCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFNLTMEWWNDL
WLNEGFAKFMFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMGDG
FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
TGLLKGTHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
MYKLMEKRD MNVETQFKAFILRLRLDIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV
QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALC
RTQNKEKLQWLLDESFKGDKIKTQEFQILTILGRNPVGYPLAWQFLRKNWNKLVQKFELGS
SSIAHVMGTTNQFSTRTRLEE VKGFSSSLKENGSQLRCVQQT IETIEENIGWMDKNFDKIR
VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATGGGCCCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG
GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTC
CTACCTGTGTGCAGCCCCCTTGGAACTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
GAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGGTTTGGCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCA
AACTGGGGAGAGCCTGGAGCATCCGGAAGTGGCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

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FIGURE 250

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVVWVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVC
PSC

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVVWVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVC
PSC

FIGURE 251

CGGACGGGCAGGACGCCCCGTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCGCT
CAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAAGAGTCG
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCGTGTCAT
GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
CGCCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCCAAGGACGAGGCTGCCA
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGAGATGGTGGCCT
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
GAGAACATGTGAGCCTCAGGCTGGGGCTGCCCATTTGGGGGGCCCCACATGTCCCTGCAGGGTT
GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
AAAGTGTTCCCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC
TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 252

M R G N L A L V G V L I S L A F L S L L P S G H P Q P A G D D A C S V Q I L V P G L K G D A G E K G D K G A P G R P G R V G
P T G E K G D M G D K G Q K G S V G R H G K I G P I G S K G E K G D S G D I G P P G P N G E P G L P C E C S Q L R K A I G E
M D N Q V S Q L T S E L K F I K N A V A G V R E T E S K I Y L L V K E E K R Y A D A Q L S C Q G R G G T L S M P K D E A A N
G L M A A Y L A Q A G L A R V F I G I N D L E K E G A F V Y S D H S P M R T F N K W R S G E P N N A Y D E E D C V E M V A S
G G W N D V A C H T T M Y F M C E F D K E N M

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
TTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGT
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCA
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT
CCTACATTAAAAATATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTTTGCATATGAA
AA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCCTGTGCCTGCTGTGCC
CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
GAGCCCTGCGGAGAGCTCAAGCGCCCAGCTCTGCCCCAGGAGCCCAGGCTGCCCCGTGAGTC
CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTGGGTGGTGTATCCCCCTGGGGC
TGCTGTTCCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACTCTCTTAGAGGAG
CTGCTCAGCAAATACCAGCACAAACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA
GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGCAGAGGCTGGCACCCGGGGGTGGGGC
CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCGTGTGATGG
CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTGTGTTT
TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
AAACCTTAGACTCCCGGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG
GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
TGCCCAGGCTGGTCTTGAACTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
CTAGGATTATAGGCATGAGTCACCCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGGCCCAGGG
CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTC
CTTAGCCCGTGTGAGCCTCACTTTCCACTTGAGAGTCCCTTCCTCGCGTGGTTGCCATGACT
GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
CTTTGCTAACC GGGAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCTCCCGGGT
GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
TGGAACCTTCCTTCCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGCCCATCCGTCAGCTATGAATGGCTT
TTTAAACAAACCCACGTCCCAGCCTGGGTAACATGGTAAAGCCCCGTCTCTACAAAAAATC
CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAAA

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FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

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FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATGGG**
GTCTGGGCTGCCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCCACCTCCTGAGTGGCAATAAATAAAATTCTGGTATGCTG

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FIGURE 258

MGSGPLVLLLTLLGSSHGTGPGMTLQCLKESFLTNSSESSFELLEKLCLLLHLPSGTS
VTLHHARSQHHVVCNT

FIGURE 259

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTTGAAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCTCTCCC
CTCCGATTGTTCTAAATTAATTGAAAGATGTCTGCTGTGGAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGG**ATGAT**GGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCTTGCAGCTTTTCTGCCCCCGCCGAGTGTAC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGAGCAAGGGCTGG
 AAAAAATGTACCCAAGCAACGAGGGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAAATATA
 TCTGTCATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT
 GGCCTGAGAGTTGAACGTGCCAACGGGAGATTGACTACATAACAATACCTTCGAGAGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGATGAAAGATGCTGTCTATA
 ACTCTCCAAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAC
 ATACGGGCATTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAGGTTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAATATAACCTGCAGAAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTGATGGGATACCCCATGCAGAAGCCAG
 GATGCTGAAGCCTCATTCTCTTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC
 CCAACTTGTTCCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCCTGGAATGAAGGAAACCAGATCATTTACAACTCCAGACAAAGAGAAA
 GCTGCCTCTGAAG**TAA**TGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTT
 TACAGGACAGTGAGGCTATAGCCCCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGAAATACGTATGCCTCCTTTTCCCAAATGTCACTGCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTCTTTACT
 GCTCCCCAGCATTTACTGTAACCTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGC
 CCCTAATATTACCACTGGCTTTTCTCTCCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAATACTATTAATATTTCTTT
 CTTTTCTTTTCTTTTTTTTTTGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTCC
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAATACTATTTCTTATTGAGGTTTAACTCTATTTCCCTAGCCCTGTC
 CTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAATATTAACATTTGAATATCGCTTT
 CCAGGTGTGGAGTGTGTCACATCATTGAATTCTCGTTTTACCTTTGTGAAACATGCACAAG
 TCTTTACAGCTGTCATTCTAGAGTTTAGGTGAGTAACACAATTACAAAGTGAAAGATACAGC
 TAGAAAATACTACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAATACGTATGTT
 TGTTACCTACTCTTATAGTCAATGCGTTCATCGTTTCAGCCTAAAAATAATAGTCTGTCCC
 TTTAGCCAGTTTTCATGTCTGCACAAGACCTTTCAATAGGCCTTTCAAATGATAATTCCTCC
 AGAAAACCAGTCTAAGGGTGAGGACCCCACTCTAGCCTCCTCTTGTCTTGCTGTCTCTGT
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVLFLLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAEKKKIRTLNLASCDNMLMGIKSLKIVKKMMDTHGSMKDAVYNPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLEFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

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FIGURE 263

GGGCGCCCGCGTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC**ATG**GAGCTCTCGCAGA
TGTCGGAGCTCATGGGGCTGTCGGTGTTGCTTGGGGCTGCTGGCCCTGATGGCGACGGCGGCG
GTAGCGCGGGGGTGGCTGCGCGCGGGGGAGGAGAGGAGCGGCCGGCCCGCCTGCCAAAAAGC
AAATGGATTTCCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTC
GGAAGGAGAAGCCTCAACAACACAACCTTCACCCACCGCCTCCTGGCTGCAGCTCTGAAGAGC
CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGC
AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCCTGCAGCGAGAGCACCGCAGCA
TGAGAGCCAACGTGGAGCTGGACCACGCCACCCCTGGTGCCTTCAGCCCTGACTGCAGAGCC
TTCATCGTCTGGCTGGCCAACGGGGACACCCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA
TGGGGGCTACACCTTCACAGCCACCCCAGAGGACTTCCCTAAAAAGCACAAGGCGCCTGTCA
TCGACATTGGCATTGCTAACACAGGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTC
CTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACCAGATGAACAACAC
ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCCAGATGTGA
AGGTTTGGGAAGTCTGCTTTGGAAAGAAGGGGGAGTTCCAGGAGGTGGTGCAGCCTTCGAA
CTAAAGGGCCACTCCGCGGCTGTGCACTCGTTTGTCTTCTCCAACGACTCACGGAGGATGGC
TTCTGTCTCCAAGGATGGTACATGGAACTGTGGGACACAGATGTGGAATACAAGAAGAAGC
AGGACCCCTACTTGCTGAAGACAGGCCGCTTTGAAGAGGCGCGGGGTGCCGCGCCGTGCCGC
CTGGCCCTCTCCCCAACGCCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCATCTCTA
CAATACCCGGCGGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCCA
ACTTGTCTTTTGACATCACTGGCCGCTTTCTGGCCTCCTGTGGGGACCGGGCGGTGCGGCTG
TTTCACAACACTCCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
CTCCAACGAGAGCACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCCTGA
AGAGCCTGGGTGCCCTGAAGAAG**TGA**CTCTGGGAGGGCCCCGGCGCAGAGGATTGAGGAGGAG
GGATCTGGCCTCCTCATGGCACTGCTGCCATCTTTCCTCCCAGGTGGAAGCCTTTCAGAAGG
AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTTCTTCCATTGAACTACTCTTGTCTACTT
AGGTCTCTCTCTTCTTGCTGGCTGTGACTCCTCCCTGACTAGTGGCCAAGGTGCTTTTCTTC
CTCCCAGGCCCAGTGGGTGGAATCTGTCCCCACCTGGCACTGAGGAGAATGGTAGAGAGGAG
AGGAGAGAGAGAGAGAATGTGATTTTTGGCCTTGTGGCAGCACATCCTCACACCCAAAGAAG
TTTGTAATGTTCCAGAACAACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTTTGCAAGGA
TGGGAGACTGGGATAGCTTCCCATCACAGAACTGTGTTCCATCAAAAAGACACTAAGGGATT
TCCTTCTGGGCCTCAGTTCTATTTGTAAGATGGAGAATAATCCTCTCTGTGAACCTCCTTGCA
AAGATGATATGAGGCTAAGAGAATATCAAGTCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT
AGTACTATTGTCCAATGTGATGAAAGTGGTAAAAGTGGGAACCAAGTGTGCTTTGAAACCAA
TTAGAAACACATTCTTGGGAAGGCAAAGTTTTCTGGGACTTGATCATAATTTTATATGGT
TGGGACTTCTCTCTTCGGGAGATGATATCTTGTTTAAAGGAGACCTCTTTTCAGTTCATCAAG
TTCATCAGATATTTGAGTGCCCACTCTGTGCCCAAATAAATATGAGCTGGGGATTAAAAAAA
AAA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQIRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQRLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
CAGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
TCCTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGT
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCA
AGCACACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
CGCTGCTCCATGGACTTGAAGAACATCAATTTTTTAGGCGCTTGCTGGTCTCAGGATACCCA
CCATCCTTTTCCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC
TCTCCCAGTCCCTACACTGACTACCCTGATCTCTCTGTCTAGTACGCACATATGCACACAG
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG
CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
AATGGCAGAAAGGACATTCCCCCTCCCCCTCCCCAGGTGACCTGCTCTCTTTCCTGGGCCCTG
CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTTGGGCACAGGCTCTTGGGT
GCATTGCTCAGAGTCCCAGGTCCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGG
ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT
TAACCACTGAAGCCCCCAATTCCCACAGCTTTTCCATTAAAATGCAAATGGTGGTGGTTCAA
TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCCTTTCCA
AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTGAGACCAGGGAGG
CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

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FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTCTTTC
CTCCAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAA
GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
CCTCTGTGAGAGGAAGCTGCGGATCTGTCTCCTGAAAAGCATGTTGGACCAGCTGGGCG
TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
TTCAAAGGAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT
GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTTCCGAGCCTGGAACGGAG
GCTTCTCTGGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT
TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAAATGAT
TGTGTGAAACTGCCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATT
GTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTA
TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGG
TGAGCAAGTCACTTGAGGTGCGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
TCTACTAAAAATACAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

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FIGURE 268

MSFLQDPSFFTGMWWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

MSFLQDPSFFTGMWWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTCGCAGGTGCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACCTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLALGLPELLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

MANPGLGLLLALGLPELLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

FIGURE 271

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAAATTTTCAAACACAGCAGAATGACATTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

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FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEEAWGRGVKKNT

CCGAGGAATAACTAGAGGAGGAACA**ATG**GGGTTATTTCAGAGGTTTTGTTTTCTCTTAGTTCT
GTGCGTGTCTGCACCAAGTCAAATACTTCTTCATTAAGCTGAATAATAATGGCTTTGAAGATA
TTGTTCATTGTTATAGATCCTAGTGTGCCAGAAGATGAAAAAATAATTGAACAAATAGAGGAT
ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAAGATTTTTTTTCAAAAA
TGTATCTATATTAATTCTTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAAACATG
AAAACCATAAACATGCTGATGTTATAGTTGTCACCACTACACTCCCAGGTAGAGATGAACCA
TACACCAAGCAGTTTACAGAAATGTGGAGAGAAAAGGCGAATACATTCACTTCACCCCTGACCT
TCTACTTGGAAAAAAACAAAATGAATATGGACCACCAGGCAAACCTGTTTGTCCATGAGTGGG
CTCACCTCCGGTGGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTTCTACCGTGTCTAAC
TCAAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAAATAGAGTTTATA
GTGTCAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACCTGATG
GAAAAGATTGTCAATCTTTCTGTATAAAGTACAACAGAAAAAGCATCCATAATGTTTATG
CAAAGTATTGATTCTGTTGTTGAATTTTGTAACGAAAAAACCCATAATCAAGAAGCTCCAAG
CCTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAATTTCTGAGGATT
TTAAAAACACCATAACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTGCTGAAGATC
AGTCAAAGAATTGTGTCTGTTAGTTCTTGATAAGTCTGGAAGCATGGGGGTAAAGACCGCT
AAATCGAATGAATCAAGCAGCAAAAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGG
TGGGGATGGTTCACCTTTGATAGTACTGCCACTATTGTAAATAAGCTAATCCAAATAAAAAGC
AGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGAACCTCCAT
CTGCTCTGGAATTAATATGCATTTTCAGGTGATTTGGAGAGCTACATTTCCCAACTCGATGGAT
CCGAAGTACTGCTGCTGACTGATGGGGAGGATAAACACTGCAAGTCTTGATTGATGAAGTG
AAACAAAGTGGGGCATTGTTTATTGTTTTGTTTTGGGAAGAGCTGCTGATGAAGCAGTAAT
AGAGATGAGCAAGATAACAGGAGGAAGTCATTTTTATGTTTCAGATGAAGCTCAGAACAATG
GCCTCATTGATGCTTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAAGTCCCTT
CAGCTCGAAAGTAAGGGATTAACACTGAATAGTAATGCCTGGATGAACGACACTGTCATAAT
TGATAGTACAGTGGGAAGGACAGTCTTTCTCATCATGGAACAGTCTGCCTCCCAAGTA
TTTCTCTCTGGGATCCAGTGGAAACAATAATGAAAATTTACAGCTGGATGCAACTTCCAAA
ATGGCCTATCTCAGTATTTCCAGGAACCTGCAAAGGTGGGCACCTTGGGCATACAATCTTCAAGC
CAAAGCGAACCAGAAACATTAACATTTACAGTAACCTTCTCGAGCAGCAAATTTCTTCTGTGC
CTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAAACAGTTTCCCCAGCCCCAATGATT
GTTTACGCGAAATTTACAAAGGATATGTAACCTGTTCTTGGAGCCAAATGTGACTGCTTTTAT
TGAATCAGCAAGATGGACATACAGAAGTTTTTGGAACTTTTGATAATGGTGCAAGGCTGATT
CTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAAATGGCAGATAT
AGCTTAAAAGTTTCGGGCTCATGGAGGAGCAAACACTGCCAGGCTAAAATTACGGCCTCCACT
GAATAGAGCCGCGTACATACCAGGCTGGGTAGTGAACGGGGAAATGAAGCAAACCCGCCAA
GACCTGAAATTGATGAGGATACTCAGACCCTTTGGAGGATTTACGCCGAACAGCATCCGGA
GGTGCAATTTGGTATCACAAGTCCCAAGCCTTCCCTTGCTGACCAATACCCACCAAGTCA
AATCACAGACCTTGATGCCACAGTTCATGAGGATAAGATTATTCTTACATGGACAGCACCAG
GAGATAATTTTGATGTTGAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATTCTT
GATCTAAGAGACAGTTTTTGATGATGCTCTTCAAGTAAATACTGATCTGTCAACCAAGGA
GGCCAACTCCAAGGAAAGCTTTGCATTTAAACAGAAAATATCTCAGAAGAAAATGCAACCC
ACATATTTATTTGCCATTAAAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACAT
GCACAAGTAACCTTTGTTTTATCCCTCAAGCAAATCCTGATGACATTGATCCTACACCTACTCC
TACTCCTACTCCTACTCCTGATAAAAGTCATAATTTCTGGAGTTAATATTTCTACGCTGGTAT
TGTCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAGTACCACCATT**TGA**ACCTTA
ACGAAGAAAAAAATCTTCAAGTAGACCTAGAAGAGAGTGTTTAAAAAACAAACAAATGTAAGT
AAAGGATATTTCTGAATCTTAAATTTTCAATCCCATGTGTGATCATAAACTCATAAAATAAAT
TTAAGATGTCGAAAAGGATACTTTGATTAAATAAAAAACACTCATGGATATGTAAAACTGT
CAAGATTAAAATTTAATAGTTTCAATTTATTTGTTATTTTATTTGTAAGAAATAGTGATGAAC
AAAGATCCTTTTTTCATACTGATACCTGGTTGTATATTTATTTGATGCAACAGTTTTCTGAAAT
GATATTTCAAATTTGCATCAAGAAATTAATTAATCATCTATCTGAGTAGTCAAATACAAGTAA
GGAGAGCAATAAACAACATTTGGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 274

MGLFRGFVFLLLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTASTY
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDL LLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNRSTWEVISNSED FKNTIPMVTPPPPPVFSLLKISQRIVCLV
 LDKSGSMGGKDRLNRMNQAAKHFLQTVENG SWVGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLT DGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKN DGVYSRYFTAYTENGRYSLKVRAHG
 GANTARLKL RPPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQT TLEDFSRTASGGAFVVSQV
 PSLPLPDQYPPSQITDL DATVHEDKIILTWTAPGDNF DVGKVQRYIIRISASILDLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLT SKVSNIAQVTLFIP
 QANPDDIDPTPTPTPTPTPTDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAAACCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATAACGTCCTCCCG
 GGCAGGGGTGACAAACAGGTGTCATCTTTTTGATCTCGTGTGGCTGCCTTCTATTTCAAGGAAAG
 ACGCCAAGGTAATTTTGACCCAGAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACC
 CCCAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTT
 GTGGTTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGA
 GGGTGGACCAGAGAAAGGAAAGGTCCCCTCTTGTCTGGCTGCACATCAGGAAGGCTGTGATGGG
 AATGAAGGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCCTTTAAAA
 GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATG
 CAAGCAGCTCCGGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGG
 GCCCCGGCTTTGAGGGATGCCACCGCTTCTGGACGATGGCTGATTCTGATGATGATGGTTCGCC
 GGGGGCTGCTTGGCTGGATTTCCCGGGTGGTGGTTTTGCTGGTGTCTCTGCTGTGCTATCTCTGT
 CCTGTACATGTTGGCCTGCACCCCAAAAGGTGACGAGGAGCAGCTGGCACTGCCAGGGCCAACAGC
 CCCACGGGGAAGGAGGGGTACAGGCCGTCTTCAGGAGTGGGAGGAGCAGCCGCAACTACGTGA
 CCACGCTGAAGCGGAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGCAGCTCAGGAA
 TGGGCAGTACCAAGCCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAG
 GCCGACCTCCTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGG
 CCACAGAGTATGCAGCAGTGCCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGTGGAGACTGG
 CTTTACCCGCCACCCGAGGAGAGCCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGAAAGCCATT
 GAATCAGCCTTGGAGACCTGAACAATCCTGCAGAGAACAGCCCCAATCACCGTCTTACACGGCCT
 CTGATTTTCATAGAAGGGATCTACCGAACAGAAAGGGACAAAGGGACATTGTATGAGCTCACCTTCAA
 AGGGGACCACAAACACGAATTCAAACGGCTCATCTTATTTGACCATTCAGCCCTCATGAAAGTG
 AAAAATGAAAAGCTCAACATGGCCAAACAGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGTGG
 ACAAGTTCGGCAGTTTCATGCAGAATTTAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCT
 CACTGTTGTTTACTTTGGGAAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAAAACACTTCCAAA
 GCTGCCAACTTCAGGAACCTTACCTTCATCCAGCTGAATGGAGAATTTTCTCGGGAAAGGGACTTG
 ATGTTGGAGCCCGCTTCTGGAAGGGAAGCAACGTCCTTCTCTTTTTCTGTGATGTGGACATCTACTT
 CACATCTGAATTCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAAGGTATTTTATCCAGTT
 CTTTTAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAAACAGC
 AGCTGGTCATAAAGAAGGAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTCAATCTG
 GTCAGACTTCATCAATATAGGTGGGTTTGTCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCAC
 CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCCTGTGCGAGGACTCTCCACC
 TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCCGAGCAGTACAAGATGTGCATGCAGTCCAA
 GGCCATGAACGAGGCATCCACCGCCAGCTGGGCATGCTGGTGTTCAGGCACGAGATAGAGGCTCAC
 CTTGCAAAACAGAAACAGAAAGACAAGTAGCAAAAAAACA**TGA**ACTCCCAGAGAAGGATTGTGGGAGA
 CACTTTTTCTTTCTTTTGCAATTACTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAAGGACG
 ACAAAGAATTTGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTGTTGGGCTTTTTAC
 AACAGAAATCAAAATCTCCGCTTTGCTTGCCTTGCAAAAGTAACCCAGTTGCACCCCTGTGAAGTGTCTGACA
 AAGGCAGAATGCTTGTGAGATTATAAGCCTAATGGTGTGGAGTTTTGATGGTGTGTACAAATACACT
 GAGACCTGTTGTTTTGTGTGCTCATTGAAATATTCATGATTTAAGAGCAGTTTTGTAAAAAATTCAT
 TAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGAGCCTATCAGCAGGGCTTAGTTTCTAGG
 AATGCTAAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTATTATGATACTAGTGAGTACATTAAGTA
 AAATAAAATGGACCAGAAAAGAAAAGAAACCATAAATATCGTGTCAATATTTCCCAAGATTAACCA
 AAAATAATCTGCTTATCTTTTGGTTGTCTTTTAACTGTCTCCGTTTTTTTTCTTTTATTTAAAAAT
 GCACTTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCCTTTGCAAGCCTTACAAGAGA
 GCACAAGTTGGCCTACATTTTATATTTTTTAAGAAGATACTTTGAGATGCATTATGAGAACTTTCA
 GTTCAAAGCATCAAATTGATGCCATATCCAAGGACATGCCAAATGCTGATTCTGTGAGGCACTGAAT
 GTCAGGCATTTGAGACATAGGGAAGGAATGGTTTGTACTAATAACAGACGTACAGATACTTTCTCTGAA
 GAGTATTTTGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGACACTTTCTGCTTTACAGAA
 AAGGAAACTCATTCAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCACATTTTCTCCTCA
 GAAGTAGGGACCGCTTTCTTACCTGTTTTAAATAAACCAAAAGTATACCGTGTGAACCAACAATCTCT
 TTTCAAAACAGGGTGTCTCCTCGGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAAATATATATAT
 ATATATATATATTGTGAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTTTGTCTACAT
 GTTATCCACCCAGGCCAGGTGGAAGTAAGTGAATTTTTTTAAATTAAGCAGTTCTACTCAATCA
 CCAAGATGCTTCTGAAAATTGCAATTTTATTACATTTCAAACATTTTTTTAAAAATAAATACAGTTA
 ACATAGAGTGGTTTTCTTCAATTCATGTGAAAATTTATTAGCCAGCACCAGATGCATGAGCTAATTATCT
 CTTTGGCTCTTCTGCTTCTGTTGCTCACAGTAACCTATTGTTTTAAAAGCTTCAAGAACATTTCAAGC
 TGTTGGTGTGTTAAAAAATGCATTGTATTGATTTGTACTGGTAGTTTATGAAATTTAATTAACAC
 AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRRDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMANLTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSEQYNPGIIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

FIGURE 277

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACC
AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT
ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC
AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAACT
CTGGAATTTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCCTCTGATCCCCCTGGACATGAAGGG
GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
TGTTCTGCTTCCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
CCAAGAGCAGATCATATATTTTGTTCACCATTCCTTCTTTTGTAAATAAATTTTGAATGTGCT
TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC
TCAAAATATTCTAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
TAGTTATTGATTTAAGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTC
AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
TGAAAATGGATCCTTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
TGAGAAGTAATTATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGGAATT
TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC
AATTCTATTTGTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG
TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSWFVVTDP SKNHTLP AVEVQSAIRMNKNRINNAFFLNDQTL E
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIAL LILSGIWQRRRKNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMP S

FIGURE 279

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG
GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC
TCGGTTAAAATGCACCTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
TGCCTCCATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
CGTTTCTCTGAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA
GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
TTTCCAACCAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCTAGA
GTGTAAATTTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCTTAA
GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
AATTTGTCTGTTACATTTCTTTTACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
ATGTGTTTACTCTCTTCTTCCCTTCCCACATTCTCAATTAAAAGGTGAGCTAAGCCTCCTCGGTG
TTTCTGATTAAACAGTAAATCCTAAATCAAAGTGTAAATGACATTTTTATTTTTATGTCTC
TCCTTAACCTATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT
TTTGTCTG

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FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKEEERLNQEKVSVYLEDTD

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACTATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCTT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACCTATTCATGCTTCCTGTGATTTT
ATCCAACTACTTACCTTGCCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTAT
TAASTTARKDIPVLPKWVGDL PNGRVCP

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG**TAA**ACCACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTTACCACATTAGCAATTAAAACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLLCCWPVGVARGGALCQ

FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG
GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCCAGGAACTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCCAGCCTGAATCTGCCTGGATGGAAGTGA
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTCATGCCTACACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTL LFHGTLLQLGQALNGVYRTTEGR LTK
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQERLHTAALPA

FIGURE 287

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCAT
CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA
AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
TGGACAGAAGTCAATGCCTTGAAGGAAATTCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACTCCGACGAAATCAACGCC
CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCCTCAACTGGG
ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACGTGTGCCTGTTCTCCCAATCAGCTCAG
GGCAAGTGGAGTGATGAGGCCTGTGCGCAGCAGCAAGAGATACATATGCGAGTTCACCATCCC
TAAATAGGTCCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTTCATGA
TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAAAAAATTGCAACACAAGATCAAT
GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGGCCCT
TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
AAACAGACTAAAATCTTTCTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAAA
AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACC
TTGTCAGCCCATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGTCT
GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
TACCCTTTTTTTTGGAAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTTGAT
CAATTTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAACCCCTAAGGCATAT
CAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTTT
AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT
TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAGTCTATTATGGGCAACCAATCTT
TGGAAGCTGAAAACGAATTTAAAGAATGCTATCTTGGAATTTGCATACGTCTGTGCAATT
TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT
TAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTAGAAAGCAAACAATTTT
AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
CCCACTTTGCAAACTTTAACTACACATGCTTGGAATTAAGTTTTAGCTGTTTTCATTGCTCA
ATAATAAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQ GK
WSDEACRSSKRYICEFTIPK

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FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC
CCCGAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
GCTCCGCTGCTGCTTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGC**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAFLVGSAPVAPVAALESAAEAGAGTLANPLGTLPKLLLS
SLGIPVNHLEGSQKCVAELGPQAVGAVKALKALLGALTVEFG

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FIGURE 291

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT
 CCTTGGCCTCCGCAGCCGATCAC**ATGA**AGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCCAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTTCAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAACCT
 GGGCCTCTCACAGGGGAGTTTTGCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTCCCAAACCT
 GTTTGATGAGATTAATCCTGAAACCAAATTAATTCTTGTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCCATTTGACCCTGTCTTCACCGAAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAA
 TTTTCGTTGTTCATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAAACCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCCTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAC
 TGCTTATTCCATGCCTCCTGTTCATCAAAGTGGACCGGCCATTTTCATTTTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTAT**TAA**ATTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCCTTTTGTCTTAACTAGTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGCTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAATTCA
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCCATCCCACTACTCAGAATGGCATGC
 TGCTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTTTCATTTAATGTTTTTGGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAAA
 GCATTAAATTGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

FIGURE 292

MKVVPSSLILLSVLLAQVWLVPGLAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEKAGE
EEKAWLMASRQQLAKETSNFGFSLLRKISMRHDGNMVFSPFGMSLAMTGLMLGATGPTETQI
KRGLHLQALKPTKPGLLPSTFKGLRETLNRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYF
DTECVPMNFRNASQAKRLMNHYINKETRGIKPLFDEINPETKLILVDYILFKGKWLTFFDP
VFTEVDTEHLDKYKTIKVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHL
ALEDYLTDDLVTWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRIFFSPFADLSELSA
TGRNLQVSRVLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDPRPFHFMIEETSGMLLF
LGRVVNPTLL

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FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCCTGAGTCCC
GAGCCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCCAGCAGGCAAA
AAAAAAAAAAAAAAAAA

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FIGURE 294

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCGGGATT
TGTTCAAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGG
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACCATGTTGGTTA
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTACCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYSYPYQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPOQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

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FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCG
CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCC
ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAAC
CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
TACACCCAAAACAACAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCAT
TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA
ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAACAATATTCT
CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTGGAAATAAACATCTGGATCTTATAGACCGT
TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCT
GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
TGCCATCTGGGCATACAAATAAGAAGTTTGTCACAGCACTCAGGATTTTGGGTATCTTTTGT
AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

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FIGURE 298

MGLGARGAWAALLLGTLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

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FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCG**ATG**GCGACCCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGC
 GCAGCTGTCAGACGCCGCCAAGAATTTTCAGAGATGTCAGATGTAAATGTATCTGCCCTCCCT
 ATAAAGAAAATTTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCCTCAGC**TAA**TTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAAGAACTGACTGGGTTTTGCTGGGTTTTCATTTTAATACCTTGTTGATTTACCAACT
 GTTGCTGGAAGATTCAAAACCTGGAAGCAAAAACCTTGCTTGATTTTTTTTTCTTGTTAACGTA
 ATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTG
 TGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTTACCCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
 TTGTTGTTGTTTTTTGTTTGTGTTTGTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGT
 AACAACTTTTTTCAAGTCACCTTACTAAACAACTTTTTGTAAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCCTGACTGTATTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGAT
 CTAAAATGCCTGGTGGCTTTTCACAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGACACT
 TGCAATAAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACT
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTTATTGGATAACTGGCTTTTT
 TCTTCCTATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA

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FIGURE 300

MATLWGGLLRLGSLLSLSCALSLLLLAQLSDAAKNFEDVRCKCICPPYKENS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMVYLT
VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLRSSRANVLNKVEYAQQRWKLQVQEQ
RKSVFDRHVVLS

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCTGGCTCTGTGCTGCTGCTGCCCCAAGGCCTTCCTGTCCCGCGGGAAGCGG
CAGGAGCCGCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATGA¹AAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAA²AACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCA³GTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTGCC⁴CCAAAATTCACA⁵ACTAACAAGGCAGA⁶ACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

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FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPPTPEGKLGRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRIILI
ILHQ

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
 GGATTTGAAAGTTGAGAGCAGC**ATG**TTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTAC
 TGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTG
 GGTGATTTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
 AGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTATGC
 AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTTCAGATGGGATGTGTTTTCCAG
 AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTCTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGG
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA
 GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTT**TGA**GAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCTCCTGTGTGTGTCCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTC
 CCAGCTGTCCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTT
 GGATCAGACCCTCCTGTGGGCAGGGTTCTTAGTGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKL RMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLLPVLILIVKKT CGNKSSVNSTV
LVKNTKKTNP EIKEKPC HFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNN SLEKKSGGGMPKTQQAF

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FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGCAGAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA
GGATGAAGATGGATACATCACCTTAAATATTAAAACCTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTCTGGGCTGGTGGCTCTGGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCTGGATTATCTCGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG
AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

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FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMF EFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

FIGURE 307

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCCGCGATCCCGG
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCCGAGTGCGGAGAA
GCCCCGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCCGG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTCACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGG
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVSFVKLFGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCT
CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTTCTGACATTGGCAGTG
CCCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
AAGAGTGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA
ACCACGTCTTGGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACTGGCTGCT
GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG
CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAG
CGCGCTCCGGGCGCCTGCCGTTTTGGGGGTGTCTCCTCCCGGGGCGCT**ATG**GCGGCGCTGGC
CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCCGGGGGCAGCCGGCCGGTGTCCG
CGCAGCGGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCCGCGCGGGCCGACCGCGGCCCCGAGCCTCA
GCTCAAAGGCATCGTCACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
ACGGAAGCATCCAGGGCACCCCAGAGGATAACCAGCTCCTTCACCCACTTCAACCTGATCCCT
GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
TTGAGAATTACTACGTCTGTACGCCTCTGCTCTTACCGCCAGCGTCGTTCTGGCCGGGCC
TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAA
GGCAGCTGCCCACCTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCC**TGA**AATGTAGTCCCTGGACTG
GAGGTTCCCTGCACTCCCAGTGAGCCAGCCACCACCACAACCTGT

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FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIIVTKLFCRQGFYLAQNPDGSIQGTPEDTSSFTFENLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDPRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQMHDPGALDGTKDDSTNSTLENLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAT
 GAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG
 AAATAAACAGAGTTAGACCCGCGGGGGTTGGTGTGTTCTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCC
 CTCCCCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTACAAAAGAAAAAGTATGTTTCATTT
 TTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA
 AGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAAAGAGGAGAGGAAATTAATAATACATCTGC
 AAAGAAATTTTCAAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCA
 CAGTTGGATTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTTAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTCTTAACCACCTGGATTTCCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAATTCCAGAAGGACCAACACCAGATAAATTATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAACAGGGCCCTATTTGACCCCT
 GCTTGTGGTGTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCAGGGCTCAGACCTGCCCTTCTGTGT
 GCTCCTGCAGCAACCAGTTCAAGCAAGGTGATTTGTGTTTCGGAACCTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAG
 GCACTTGGAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTCTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAA
 CTGAAGGAGCTCTGGTTGCGAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTTAACAGAATTCCTTCTTT
 GCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTTATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAAC
 TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACCTAGATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAAC
 GTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACCTAGTGGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGAGCGGATACAT
 TTACATCACAACCTTTGGAACCTGTAACCTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTC
 GAACACAGCTTGTTGTGCCCCGTGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACCTGAAGGCATGGCAGCT
 GAGCTGAAATGTGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA
 TGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTACGTTAAATTTACAAATGTAACCTGTGCAAGATA
 CAGGCATGTACACATGTATGGTGAGTAATCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCA
 GCAACCACTACTCCTTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
 GACCACAGATAACAATGTGGGTCCCCTCCAGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAAGGTGACAGAGAAAACCTTCACCATCCAGTGACTGATATAAACAGTGGGATCCCAGGAATT
 GATGAGGTCATGAAGACTACCAAAATCATCATTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAACAGTTAACACAATAAATTCATACAC
 CAGTTCAGTGCATGAACCGTTATTGATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAAATCTAAACA
 TTTACAGAGTTACAAAAACAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAACAAAAAGAAAGAAATTTATTTATTAATAAATTCATTG
 TGATCTAAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYNL LAMCNLREIPNLTP LIKLDLDEL DSGNHL SAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIH LHHNPWNCNCDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASLTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNVGN
TTASATLNVTAATTTTFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKFTTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRQHHRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCGCGCCAGCTCGCCCCAGGTCCGTCCGA
 GCGCCCCGGCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
 GGG**ATG**TCCCTCCTCCTTCTCCTCTTGCTAGTTTCTTACTATGTTGGAACCTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACCTTGGCCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTGAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT
 GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA
 CCAGTGACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT
 ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
 ATTTTCCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT
 CCTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCTCCACTCGCTCCACAGCAAAT
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
 CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
 ACGGTCT**GTA**ATTACAATGGACTTGACTCCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTGCACGGAACAGATTCAGATGAGCATTTTCTTATAACAATACCAACAAGCAAA
 AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
 AGGTGAATATACCTAAAACCTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAAATT
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACCTATTGGATT
 ATTAGTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
 TGAGCTAACCACCTTCTAAGAAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
 TTCATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCCAAAATAAC
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCATCTTCATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCCTCAAAT
 CAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT
 TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA
 CCAACATACCATTTAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

316/330

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHCHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

CCGAGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCCGCTACCTGCAGCCGCCGCCACGGCACGGCAGCCA
CC**ATG**GCGCTCCTGCTGTGCTTCGTGCTCCTGTGCGGAGTAGTGGATTTGCCAGAAGTTTGAGTATCACTACT
CCTGAAGAGATGATTGAAAAAGCCAAAGGGGAAACTGCCTATCTGCCATGCAAATTTACGCTTAGTCCCGAAGA
CCAGGGACCGCTGGACATCGAGTGGCTGATATACCCAGCTGATAATCAGAAGGTGGATCAAGTGATTATTTTAT
ATTCTGGAGACAAAATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTACATTTTACGAGTAATGATCTC
AAATCTGGTGATGCATCAATAAATGTAACGAATTTACAACCTGTGCAGATATTGGCACATATCAGTGCAAAGTGAA
AAAAGCTCCTGGTGTTCGAAATAAGAAGATTCATCTGGTAGTTCCTTGTTAAGCCTTCAGGTGCGAGATGTTACG
TTGATGGATCTGAAGAAATTGGAAGTGACTTTAAGATAAAATGTGAACCAAAGAAGGTTCACTTCCATTACAG
TATGAGTGGCAAAAATTGTCTGACTCACAGAAAATGCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT
ATCTGTAAAAAATGCCTCTTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC
AGTGCCCTGTTGCGTCTAAACGTTGTCCCTCCTTCAAATAAAGCTGGACTAATTCGAGGAGCCATTATAGGAAC
TTGCTTGCTCTAGCGCTCATTGGTCTTATCATCTTTTGCTGTCGTAATAAGCGCAGAGAAGAAAAATATGAAAA
GGAAGTTTCATCAGATATCAGGGAAGATGTGCCACTTCCAAAGAGCCGTACGTCCACTGCCAGAAGCTACATCG
GCAGTAATCATTTATCCCTGGGGTCCATGTCTCCTTCCAACATGGAAGGATATTTCAAAGACTCAGTATAACCAA
GTACCAAGTGAAGACTTTGAACGCACCTCCTCAGAGTCCGACTCTCCACCTGCTAAGTTCAAGTACCCTTACAA
GACTGATGGAATTACAGTTGTA**TAA**ATATGGACTACTGAAGAATCTGAAGTATTGTATTATTTGACTTTATTTT
AGGCCCTCTAGTAAAGACTTAAATGTTTTTTAAAAAAGCACAGGCACAGAGATTAGACGAGCTGTAAGAACAC
ATCTACTTTATGCAATTGGCATTAGACATGTAAGTCAGATGTCATGTCAAATTTAGTACGAGCCAAATCTTTGT
TAAAAAACCCCTATGTATAGTACACTGATAGTTAAAGATGTTTTATTATATTTTCAATAACTACCACTAACAA
ATTTTTAACTTTTTCATATGCATATTCTGATATGTGGTCTTTTAGGAAAAGTATGGTTAATAGTTGATTTTTCAA
AGGAAATTTTTAAATTTCTTACGTTCTGTTTAAATGTTTTTGCTATTTAGTTAAATACATTGAAGGGAAATACCCG
TTCTTTTTCCCCTTTTTATGCACACAACAGAAACACGCGTTGTGTCATGCCTCAAACATTTTTTTATTTGCAACTACA
TGATTTACACAATTCTCTTAAACAACGACATAAAATAGATTTCTTGTATATAAAATACATTACATCGCTCCA
TAAAGTAAATTTCTCAAAGTGCTAGAACAATCGTCCACTTCTACAGTGTTCTCGTATCCAACAGAGTTGATGC
ACAATATAATAACTACGAGTCCAATATTAATAAACTTAGGCACCTGACTAACTTTAATAAAATTTCTCAAAC
TATCAATATCTAAAGTGCATATATTTTTTAAGAAAGATTATTCTCAATAACTTCTATAAAAAATAAGTTTGATGG
TTTGGCCCATCTAACTTCACTACTATTAGTAAGAACTTTAACTTTTAATGTGTAGTAAGGTTTATTCTACCTT
TTTCTCAACATGACACCAACACAATCAAAAACGAAGTTAGTGAGGTGCTAACATGTGAGGATTAATCCAGTGAT
TCCGGTCACAATGCAATCCAGGAGGAGGTACCCATGTCACTGGAATTTGGCGATATGGTTATTTTCTTCCC
TGATTTGGATAAACCAAATGGAACAGGAGGAGGATAGTGATTCTGATGGCCATTTCCCTCGATACATTCCCTGGCTT
TTTTCTGGGCAAAGGGTGCCACATTGGAAGAGGTGGAATATAAGTTCTGAAATCTGTAGGGAAGAGAACACAT
TAAGTTAATTCAAAGGAAAAAATCATCATCTATGTTCCAGATTTCTCATTAAGACAAAGTTACCCACAACACT
GAGATCATATCTAAGTGACACTCCTATTGTGAGGTCTAAATACATTAAAAACCTCATGTGTAATAGGCGTATAA
TGTATAACAGGTTACCAATGTTTTCTGAATGCATAAAGAAATGAATAAACTCAACACAGTACTTCTTAACAA
CTTCAACCAAAAAAGACCAAAACATGGAACGAATGGAAGCTTGTAAGGACATGCTGTTTTAGTCCAGTGTTTT
CCACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATACAAAACATTGGAGCTGGAGGCCATTATCCTT
AGCAAACATAATGCAGAAACAGAAAATCAACTACCGCATGTTCTCACTTATAAGTGGGAGGTAATGATAAGAACT
TATGAACACAAAGAAGGAAACAATAGACATTGGAGTCTATTTGAGAGGGGAGGTTGGGAGAAGGAAAAGGAGCA
GAAAAGATAACTATTGAGTACTGCCTTTCACACCTGGGTGATGAAATAATATGTACAACAAATCCCTGTGACACA
TGTTTTACCTATGGAACAAACCTTCATGTGTATCCCTAAACCTAAAATAAAAGTTAAAAAARAAAAA
AAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA
AAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDFAFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHVLVVLVKPSGARCYVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL
ALALIGLIIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC
CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
AGAGATGAAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTG
CTTCTCTGGAGCCAGGTATCAGGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT
GAAGGGGGTGTTCCTCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
CTCAGGATAACATCACGAGTCCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAAGTGTTCACAAAA
CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC
TTGTTCTCATCGTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
AGTGCACACAGGCGGTTTTCTGCTATTCGGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGC
TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTTGTTCCCTGTGTCATTTCA
AACAGTCTCCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATT
TTGGCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTCTATTT
AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACATCCTTGCCACAGTGTGGGGCAG
TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
GTTAAAAAACAGAGAGGGATGCTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACT
GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAAGTGCATCTGTTTGAAAAG
TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT
TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCTTGCTAATAAAAGACAACATAA
CTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

320/330

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPCPPLLATASQMOMVVLPCLGFTLLLWSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACCTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACT
GTGGGAGACAGCCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGC AAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACGCGGCTACAATTAATACATAACCTTATGTATCATAACACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGGCCGCCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTTCAGAGGCAACATTTTTGGATCACACTATTTTCGAC
CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACC
CCCATAACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGT
GCTGAAGCCCCGGGCCCCGGATGACCCCGGCCCCGGCCTCCTGTTACAGGAGCTCCCGAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCTG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGY
DVIHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNVLKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGCAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGCACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
 GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCCTCAT
 GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCACAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTTC
 CTTTGCTGGGAGCTCTGCTTCCTCCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
 CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCCT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACCACAGACG**TGA**GTGCAGGTGAAAATGGAGGTTTCCTCCTCCTGCGGCTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCACGCCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTCAGGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCCTAGCCTG
 GGCCCCCACCAGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGGCTTACCTGTTCCAGAGGTGTCCTTGGAATCACCTTGG
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
 TTTAAATTCACCTCAGTGTGGCCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
 TTVQTITGSDPEEAI FDTLCTDDSS EEA KTLTMDILT LAHTSTEAKGLSSESSASSD GPHPV
 ITPSRASESSASSD GPHPVITPSRASESSASSD GPHPVITPSWSPGSDVTLLAEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTL SGALVTVSRNPLEETSALSVETPSY
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPTSRD
 PLPSVPPTTTN SSRGTNSTLAKITTS AKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCCGCGG
GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA
GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAATAAGACCAGAGGGAGGATTAT
CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTTCGGGGGAGAAGGGAG
CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
GCCTCAAAAAGAGTCTAGAAGATGTTGTGATTGACATCCAGTCATCTCTTTCTAAGGGAATC
AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTTGCTGTTCAAC
AAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
GACAACCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAAGCAGTCACTCCCC
TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT
CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTTACAATTTTCTCTGATCAAGAAA
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCA
CATACCACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC
TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
AACCATAACGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCCTA
CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGCGGAAGGT
AGGGAGGCCAGTCCAGGCAGTTCTTCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC
ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCTGTTGATAGGCC
TCGTCCTCCTGGGTAGAATCCTTTTCGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTCTTTTTTTTTTTGGAGACAGAGTCTT
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTG
GTCTCAAACCTCCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG
CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGGAGAAGGAATGAAGTG
GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT
ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAA
GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGGTTCCAGATAAAATCAAC
TGTTTATATCAATTTCTAATGGATTTGCTTTTCTTTTTATATGGATTCTTTAAACTTATT
CCAGATGTAGTTCCTTCCAATTAAATATTTGAATAAATCTTTTGTTACTCAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLKGIKRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIHAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCCAGCGCCCAGAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCCTATATGCAGAAGAAGAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCTTTCCAGGACCCTGCTGTCTCCTCCCTCCCCTTCTCCCAC
 CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC
 CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGCTGCTGAGCCTTCTGTGAGC
 CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC
 CCTTCCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGATGTTCCA
 GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC
 CTCATGCCCAGTGTGCGACCCTGCCTTCCCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTCTAACAATGCCCAGTGACTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTG
 ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG
 TCCAGGCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG
 TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAATACTATTTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT
 GCTGCCCAGGCTGGAGTGCAGTGGCAGCATCTGCAAACCTCCGCCTCCTGGGTTCAAGTGATT
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCTTTAAAAAGTGAAATTAAGAGTTGTTTCAAGTATGCAAACTTGGAAG
 ATGGAGGAGAAAAAGAAAGGAAGAAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT
 TATTTCTGTTTTGTTGTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT
 TTTACAGAGCAATTATCTTGTATATACAACCTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATTCAGCACTTCTCTGTGTTTTACAGACCTTTTTATAAATAAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLQDAGEYWCGVEKRGPDESLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPPLHTSEEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128